

FIGURE 1

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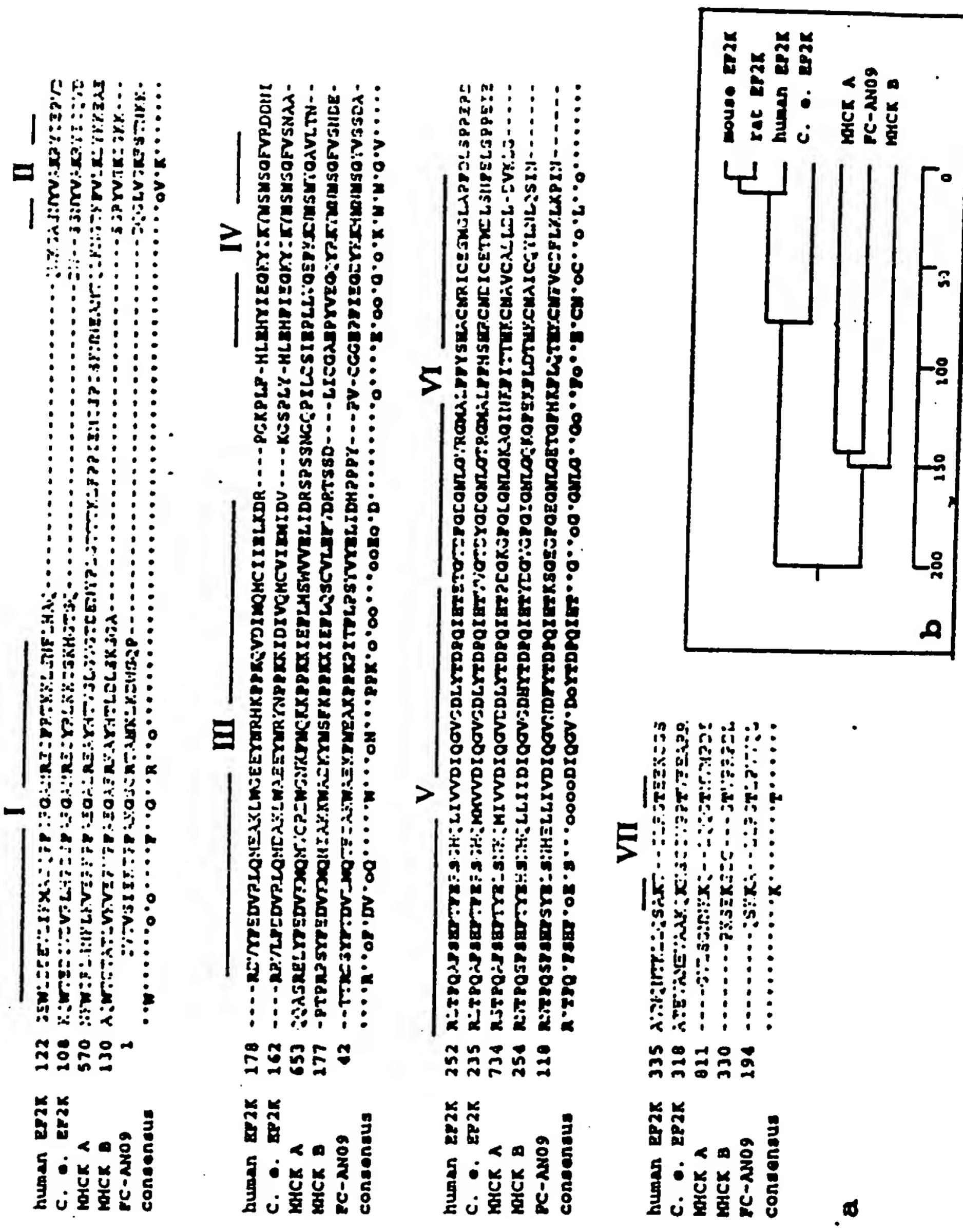


FIGURE 2

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Sequence alignment of human cEF-2K, C. elegans cEF-2K, and mouse cEF-2K with MRCK A. The alignment shows the amino acid sequence for each protein, with identical residues highlighted in black and similar residues in gray. The alignment is presented in blocks, with each block corresponding to a specific region of the protein. The sequence starts at position 1 and ends at position 734. The alignment shows high conservation between the three proteins, particularly in the N-terminal region and the C-terminal region.

Position	Human cEF-2K	C. elegans cEF-2K	Mouse cEF-2K	MRCK A
1	W	W	W	
2	Y	Y	Y	
3	Y	Y	Y	
4	Y	Y	Y	
5	Y	Y	Y	
6	Y	Y	Y	
7	Y	Y	Y	
8	Y	Y	Y	
9	Y	Y	Y	
10	Y	Y	Y	
11	Y	Y	Y	
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28	Y	Y	Y	
29	Y	Y	Y	
30	Y	Y	Y	
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220	Y	Y	Y	
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222	Y	Y	Y	
223	Y	Y	Y</	

FIGURE 3

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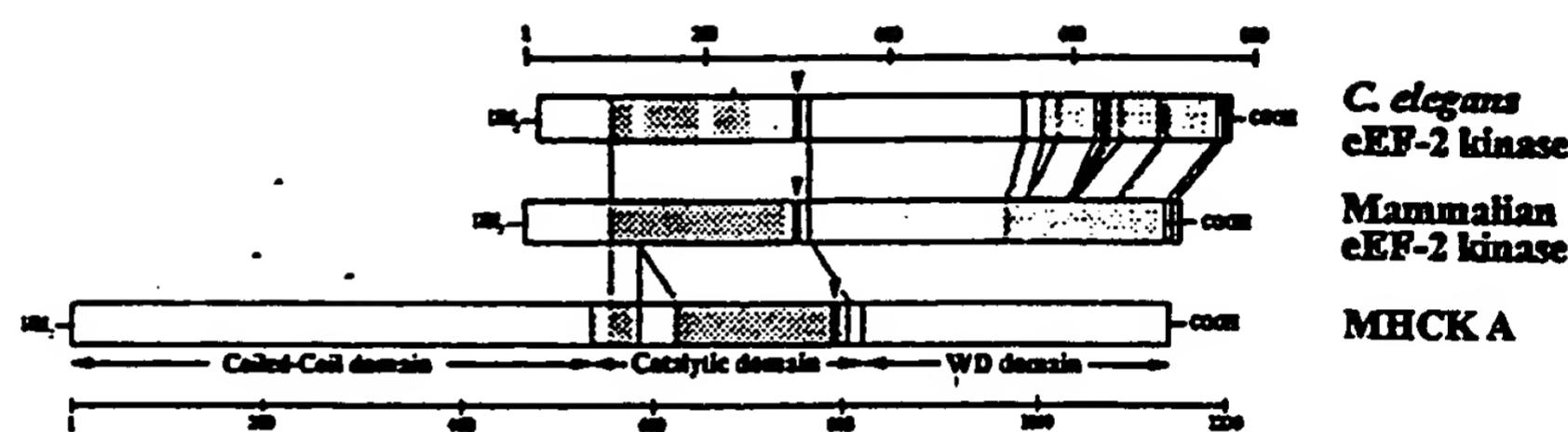


FIGURE 4

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1 cgggcgcggg cgcgtccctc tggccagtca cccggcggag ctggtcgcac aattatgaaa
61 gactcgactt ctgctgctag cgctggagct gagttagttc tgagaagggtt tcccgggct
121 gtccttgttc ggtggcccgt gccaccgcct ccggagacgc tttccgatag gtggctgcag
181 gccgcggagg tggaggagga gccgctgccc ttccggagtc cgccccgtga ggagaatgtc
241 ccaaaaatcc tggatagaga gcactttgac caagagggag tgtgtatata ttataccaaag
301 ctccaaagac cctcacagat gtctccagg atgtcagatt tgtcagcaac ttgtcagatg
361 tttctgtggc cgttggtca agcaacatgc atgtttact gcaagtcttgc ccatgaaata
421 ctcagatgtg agattgggtg aacactttaa ccaggcaata gaagaatggc ctgtggaaaaa
481 gcacacggag cagagcccaa cagatgctt tggagtcatt aatttcaag ggggtctca
541 ttcctacaga gctaagtatg tgagactatc atatgatacc aaacctgaaa tcattctgca
601 acttgtgtt aaagaatggc aaatggagtt acccaaactt gttatttctg tacatggagg
661 catgcagaag ttgttaacttc atccaagaat caagcagttg cttggaaagg gtcttattaa
721 agctgcagtt acaaccggag cttggatttt aactggagga gtcaatacag gtgtggcaaa
781 acatgttggc gatgccctca aagaacatgc ttccagatca tctcgaaaaa tttgcactat
841 tggaaatagc ccatggggag tgatagaaaa cagaaatgat cttgttgggag gagatgtggt
901 tgctccttat caaaccctat tgaatccctt gagcaaattt gatgttctg ataatctaca
961 ctcccatttc atcttggtgg atgatggcac tttggaaag tatggggcag aagtcagact
1021 gagaagagaa cttgaaaaaa ccattaatca gcaaagaatt catgctagaa ttggcaagg
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1141 gtaccttcag gaaagcccccc cagttccagt tttgtgtgt gaaggacag gcagagctgc
1201 agatttacta gcctatatcc acaaacagac agaggaagga gaaaatcttc ctgatgcagc
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1321 tcatttattt caaacaatga tggagtgtat gaaaaaaa gagcttatca ctgttttca
1381 cattggatca gaggatcatc aagatataga tttggccata ctcactgcac tgctgaaagg
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1681 aggtccaaacc aatccaatgt tttccatct cattggat gtcaagcagg gtaatctccc
1741 cccgggtac aagatcactt taattgat tttcgatttgc attgagtttgc tcatggagg
1801 aacctacaga tgcacataca cacgaaaacg tttcgatttgc atatataata gtcttggtgg
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1921 tgaaaactttt ggcaatagag ctgataaaaaa gaaaaatg agacacaatc atttcattaa
1981 aacagcccaa ccctacagac caaagatggc tgcatctatg gaagaaggaa agaagaaaaag
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9781 attttttttttgc ttttttttttgc ttttttacc tatgctatttgg
9841 attttttttttgc ttttttttttgc ttttttacc tatgctatttgg
9901 attttttttttgc ttttttttttgc ttttttacc tatgctatttgg
9961 attttttttttgc ttttttttttgc ttttttacc tatgctatttgg

FIGURE 5B

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3421 cccgacaatc tgtggcctg gaacttggtt gactccattt cttcaagcag tctacctctt
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3661 ttgctgtgt tgcaaaaagaa gaaagaaaaga taagacttcc gatgggccaa aactttctt
3721 aacagaagaa gatcaaaaaga aactccatga ttttgaagag cagtgtgtt agatgtactt
3781 ttagtggaaa gatgacaaat tcaattctgg gagtgaagag agaattccggg tcactttga
3841 aagagtggag cagatgagca ttcagattaa agaagttgga gatcgtgtca actacataaa
3901 aagatcatta cagtcttttag attctcaaat tggcatctg caagatctct cagccctaacc
3961 agtagataca ttgaaaacac ttacagccca gaaagcttca gaagctagta aagtgcacaa
4021 ttagatcaca cgagaatttga gtatttccaa acacttggct cagaatctt ttagatgatgt
4081 tcctgttaaga ccttgttgg agaaacctag tgctgtaaac acactgagt cctctttcc
4141 tcaaggtgat cgggaaaagta ataatcctt tcttgtat attttatga aagatgaaaa
4201 agaccccaa tataatctgt ttggacaaga tttgcccgtg atacccaga gaaaagaatt
4261 caacattcca gaggctgggt cctcctgtgg tgccttattt ccaagtgtcg tttctcccc
4321 agaattacga cagagacgac atggggtaga aatgttaaaa atatttaata aaaatcaaaa
4381 attaggcagt tcacctaata gttcaccaca tatgtcctcc ccaccaacca aattttctgt
4441 gagtacccca tcccagccaa gttgcaaaag ccacttggaa tccaccaacca aagatcaaga
4501 acccattttc tataaagctg cagaagggga taacatagaa tttggagcat ttgtgggaca
4561 cagagatgt atggacttac agaggtttaa agaaacatca aacaaaataa gagaactgtt
4621 atctaattgtt actcctgaaa acactctgaa acatgtgggt gctgctggat atagtgaatg
4681 ttgttaagact tctacttctc ttcactcagt gcaagcagaa agctgttagta gaagagcgtc
4741 gacggaagac tctccagaag tcgattctaa agcagcttg ttaccggatt gttacgaga
4801 tagaccatca aacagagaaa tgccatctga aggaggaaca taaaatggtc ttgcttctcc
4861 atttaagccc gttttggata caaattacta ttattcagct gtggaaagaa ataacctgat
4921 gaggttgtca cagagtattt ctttcgttcc tgtacctcca cgaggcgagc ctgtcacagt
4981 gtaccgtctg gaggaggtt ctcccagtat actgaataac agcatgtctt catggctca
5041 gctaggcctc tgtccaaaaa ttgagttttt aagtaaagag gaaatggag gtggttacg
5101 aagagcagtc aaagtgtgt gtacctggtc agagcacat atcctgaagt cagggcatct
5161 ctatattcatt aagtcatattc ttccctgaggt gataaaacaca tggtaagca tttataaaga
5221 agatacggtt ctacatctct gtctcagaga aataacaacaa cagagagcag cacaaaagct
5281 cacatttgc ttaatcaga tgaaacccaa atccatacca tattctccaa gttccttga
5341 agtttctgt ttgtactgcc attcagcagg gcagtggtt gctgtagaag agtgcacgt
5401 tggtaattt agaaaataca acaacaataa tggtgatgaa atcattccta caaataactct
5461 agaagagatc atgcttagcct ttagccactg gacctatgaa tataccagag gggagttact
5521 ggtacttgac ttacaaggag tgggagaaaa cttgactgac ccatctgtaa taaaagctga
5581 agaaaaaaaaga tcctgtgaca tggttttgg ccctgccaat ctaggagaag atgcaataaa
5641 aaacttcaga gccaaacatc actgttaattc ttgctgtcga aagcttaaac ttccagattt
5701 gaagaggaat gactacacgc ctgataaaaat tatatttctt caggatgagt catcagattt
5761 gaatcttcaa tctggaaatt ccaccaaaga atcagaagca acaaattctg ttcgtctgat
5821 gttatagtgc tgagtcatgg gttttgcctt acacttcaca aaagtgtaaac tgcgttttt
5881 ctttcgggg gaattgatga tataggaaga tgtgtgcaaa atgagcttgc tggccccaca
5941 catagtctag aggtaatgtt ctcattgaaa aacgcctgga ggctgcagat gacagctgga
6001 aagtgttagc tggcagagag tcagtgtctt cggctggta agggcgggaa cttgctgct
6061 gagagtggtg gttctctcac ctggtgcaagg accattaacc aaagtcaagt ttccagattt
6121 gattggctgc tcagtcacag ccattcagct aaggaaacta aattgcgcag ctttttaaat
6181 ggctgaagtc ttccctcagg tgcgtctat gataatgatg ttagctctca actaggtgtt
6241 tgtggccacg ggagaactac tccttacaat tttgcttcac aggcatgtta caaagcctgc
6301 actgaaaaacc gtttgtcttc cctctctccc tccctctttt ccctgttagta ttgaggatca
6361 aacccaggc ctcatgaaga ccatttcta agagacattt tatttaagaa tcaactata
6421 agtctatgtt tatggataca gccagttttt gttaaacaaa acctgaattt tgcaaaaagg
6481 ttttttaaca ttatcaatg ttaagaaaaa gaaagccatg ataaataaga attaactcac
6541 tgtcaatgg gtqtttcctg tqaqqaaqqt tacagttgtt acaqccctqca qttqcataca

FIGURE 5C

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CIP

6601 tctccaaaga tttacagact tagtgtatca aatcagagtg tcatgtgagc tctcacattg
6661 aaaattctat aggaatgtgt caatgtaat tctatttctg gtacttaaga aatcagttgt
6721 tggattatcc ttatacagta tagggagatc acaatacaac tttatgccaa taaaatctaa
6781 cttaaattgcc cagatattt tgcataattt gcaacaagaa aagcttatca tttgactcaa
6841 gtttatgct ttctctttct tttcatttcc taggtactaa ttttaatttt tatttggaaag
6901 gagcagtgt aagcttaccc gtattcaata gtgtatctca tagatacaga caaggccgca
6961 gagataagct gttaaatagt gtttaatgtt gatgtggaga gaaaggtgt aatctaaaa
7021 atactataacc atatacgtt tgtatatcat taaatctta aaagaaaatta aatttattct
7081 tgtttacaaa

FIGURE 6A

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Cif

MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTASLAM
KYSDVRLGEHENQAIIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEII
LQLLLKEWQMEPLPKLVISVHGMQKFELHPRIKQLLGKGLIKAAVTTGAWILTGGVNTGV
AKHVGDALKEHASRSSRKICTIGIAPWGVIENRNDLVGRDVVAPYQTLLNPLSKLNVLNN
LHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHARIGQGVVVALIFEGGPNVILTV
LEYLQESPVPPVVCETGTRAADLLAYIHKQTEEGGNLPDAEVDIISTIKTFNFGQSE
AVHLFQTMMECMKKELITVFHIGSEDHQDIDVAILTALLKGTNASAFDQLILTLAWDRV
DIAKNHVFVYQQQWLVGSLEQAMLDALVMDRVSFKLLENGVSMHKFLTIPRLEELYNT
KQGPTNPMLFHLIRDVKQGNLPPGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIYNL
GGNNRRSGRNTSSSTPQLRKSHETFGNRADKKEKMRHNHFIKTAQPYRPKMDASMEEGKK
KRTKDEIVDIDDPETKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALVACKIYR
SMAYEAKQSDLVDDTSEELKQYSNDFGQLABELLEQSFRQDETMAMKLLTYELKNWSNST
CLKLAVSSRLRPFVAHTCTQMLLSDMWMGRLNMRKNSWYKVILSILVPPAILMLEYKTKA
EMSHIPQSQDAHQMTMEDSENNFHNIIEEEIPMEVFKEVKILDSSDGKNEMEIHIKSKKLP
ITRKFYAFYHAPIVKFWNTLAYLGFLMLYTFVVLVKMEQLPSVQEWINIAYIFTYAIK
VREVFMSEAGKISQKIKVWFSDYFNVSDTIAIIISFFVGFGLRGAKWNYINAYDNHFVA
GRЛИYCLNIIIFWYVRLLDFLAVNQQAGPYVMMIGKMVANMFYIVVIMALVLLSGVPRKA
ILYPHEEPSWSLAKDIVFHPYWMIFGEVYAYEIDVCANDSTLPTICPGTWLTPFLQAVY
LFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYHFIMAYHEKPVLPPPLIILSHIVS
LFCCVCKRRKKDKTSGPKLFLTEEDQKKLHDFFEEQCVEMYFDEKDDKFNSGSEERIRVT
FERVEQMSIQIKEVGDRVNYIKRSIQLSQSLDSQIGHLQDLSALTVDTLKTLTAQKASEASKV
HNEITRELSISKHLAQNLIDDVPRPLWKKPSAVNTLSSSLPQGDRESNNPFLCNIFMKD
EKDPQYNLFGQDLPVIIPQRKEFNIPEAGSSCGALFPSAVSPPELRQRRHGVEMLKIFNKN
QKLGSSPNSSPHMSSPPTKFSVSTPSQPSCKSHLESTTKDQEPIFYKAAEGDNIEFGAEV
GHRDSMDLQRFKETSNKIRELLSNDTPENTLKHVGAGYSECCKTSTSLHSVQAESCSRR

FIGURE 6B

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CIP

ASTEDSPEVDSKAALLPDWLDRDRPSNREMPSEGTLNGLASPFPVLDTNYYSAVERNN
LMRLSQSIPFVPPVPRGEPVTVYRLEESSPSILNNNSMSSWSQLGLCAKIEFLSKEEMGGG
LRRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQ
KLTFAFNQMKPKSIPYSPRFLEVFLYCHSAGQWFAVEECMTGEFRKYNNGDEIIPTN
TLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKAEEKRSCDMVFGPANLGEDA
IKNFRAKHHCNSSCRKLKL PDLKRNDYTPDKIIFPQDESSDLNLQSGNSTKESEATNSVR
LML

Figure 7A

601-1-098 CIP

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MSQKSWIESTLTRECIVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTASLAM
KYSDVKLGDHFNQAIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRLSYDTKPEV
ILQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKAAVTTGAWILTGGVNT
GVAKHVGDALKEHASRSSRKICTIGIAPWGVIENRNDLVRDVVAPYQTLLNPLSKLNV
LNNLHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHARIGQGVPVVALIFEAGGPNVIL
TVLEYLQESPPVPVVVCEGTGRAADLLAYHKQTEEGGNLPDAAEVDIISTIKTFNFGQN
EALHLFQTLMECMKRKELITVFHIGSDEHQDIDVAILTALLKGTNASAFDQLLTLAWDR
VDIAKNHVFVYQQQLVGSLEQAMLDALVMDRVAFKLLENGVSMHKFLTIPRLEEL
YNTKQGPTNPMLFHLVRDVKQGNLPPGYKITLIDIGLIEYLMGGTYRCTYTRKRFRLIY
NSLGGNNRRSGRNTSSSTPQLRKSHESFGNRADKKEKMRHNHFIKTAQPYRPKIDTVME
EGKKKRTKDEIVDIDDPETKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALV
ACKIYRSMAYEAKQSDLVDDTSEELQYSNDFGQLAELLEQSFRQDETAMAKLLTYE
LKNWSNSTCLKLAVAAKHRDFIAHTCSQMLLTDMWMGRMRKNPGLKVILSILVPPAI
LLLEYKTKAEMSHIPQSQDAHQMTMDDSENNFQNITEEIPMEVFKEVRILDSNEGKNEM
EIQMKSKKLPITRKFYAFYHAPIVKFWNTLAYLGFLMLYTFVVLVQMEQLPSVQEWINI
AYIFTYAIEKVREIFMSEAGKVNQKIKVWFSDYFNISDTIAISFFIGFGLRFGAKWNFANA
YDNHVFVAGRLIYCLNIIFWYVRLDFLAVNQQAGPYVMMIGKMVANMFYIVVIMALV
LLSGFVPRKAILYPHEAPSWTAKDIVFHPYWMIFGEVYAYEIDVCANDSVIPQICGP
WLTPFLQAVYLFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYHFIMAYHEKPVLPP
PLIILSHIVSLFCCICKRRKKDKTSQDGPKLFLTEEDQKKLHDFEEQCVEMYFNEKDDKFHS
GSEERIRVTFERVEQMCIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQ
KASEASKVHNEITRELSISKHLAQNLIDDGPVRPSVWKHGVVNTLSSLPQGDLESNNP
FHCNILMKDDKDPQCNIFGQDLPAPVQRKEFNPEAGSSGALFPSAVSPPELRQRLHGV
ELLKIFKNQKLGSSTSIPHLSSPPTKFFVSTPSQPSCKSHLETGTDQETVCSKATEGDN
TEFGAFVGHRDSMDLQRFKETSNKIKILSNNNTSENTLKRVSSLAGFTDCHRTSIPVHSKQ
EKISRRPSTEDTHEVDSKAALIPVWLQDRPSNREMPSEEGLTNGLTSPFKPAMDTNYYYS
AVERNNLMRLSQSIPFTPVPPRGEPTVYRLEESSPNILNNSMSSWSQLGLCAKIEFLSKE
EMGGGLRRAVKVQCTWSEHDILKSGHLYIIKSFLPEVVNTWSSIYKEDTVLHLCLREIQQ
QRAAQKLTFAFNQMKPKSIPYSPRFLEVFLYCHSAGQWFAVEECMTGEF
RKYNNNNNGDEIPTNTLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKAEEKR
SCDMVFGPANLGEDAIKNFRAKHHCNSCCRKLKPDLKRNDYTPDKIIFPQDEPSDLNLQ
PGNSTKESESTNSVRLML

Figure 7B

Figure 8A

ESAEPPLTQSDKRETSHTTAAATGRSSHADARECAISTQAEQEAKTLQTSTDVSKEGNTNCKGEGMQVN
 TLFETSQVPPDWSDPPQVQVQETVRETISSQMPAFSEPAGEEESPFTGTTISFSNLGGVHKENASLAQHSEV
 KPCTCGPQQEEKQDRDGNIPDNFREDLKYEQSISEANDETMSPGVFSRHLPLPKDARADEFREPVAVSVASP
 TDTALTLENVCDEPRDREAVCAMECCEASDQGTCTFDTIDSLVGTPVDNYSPQEICSVDDTELAEQNQKVSD
 LCSSNDKTLLEVFFQTQVSETSVCSTCKSSKDGNSVMSPLFISTFTLNISHTASEGATGENLAKVEKSTYPLAS
 TVHAGQEQQPSNSGGGLDETQLLSENNPLVQFKEGGDKSPSPSAADTTATPASYSSIVSFPWEKPTTLTAN
 NECFQATRETVTIATEVHPAKYLAVisPEDKHAGGTEERFPRASHEKVSQFPSQVQVDHILSGATIKSTKEL
 LCRAPSVPGVPHHVLQLPSEGEGFCNSNPLQVDDNLSGDKSQTVDRLRADFRSYEEENFQERGSETKQGVQQQSL
 SQQGSSLAPDFQQSLPTTSAAQEERRNLVPTAPSPASSREGAGQRSQWGTRVSVVAETAGEEDDSQALSNNVPS
 LSDILLESKEYRPGNWEAGNKLKITLEASASEIWPPRQLTNSESKASDGGLIIPDKVWAVPDSLKADAVV
 PELAPSEIAALAHSPEDAESALADSRESHKGEETPTISVHWRSLSRRGFSQPRLLSVDPVDEKELSVTDSL
 AASETGGKENVNNVSQDQEEKQLKMDHTAFFKKFLTCPKILESSVDPIDEISVIEYTRAGKPEPSETTPQGA
 REGGQSNDDGNMGHEAEIQSAILQVPCLQGTILSENRISSRSQEGSMKQEAEQIQPEEAKTAIWQVLQPSEGG
 ERIPSGCSIGQIQESSDGSLLGEAEQSKKDKAELISPTSPIMTHSSLGVDTNSTGQIHIDVPENDIVEP
 RKRQYYVFPVSQKRGTIENERGKPLPSSPDLTRFPCTSSPEGNVTDFLISHKMEEPKIEVLQIGETKPPSSSSSS
 AKTLAFISGERELEKAPKLLQDPQCQKGTLGCAKKSRREREKSLEARAGKSPGTLTAVTGSEEVKRKPEAP
 GHLAEGVKKKILSRVAALRLKLEEKENIRKNSAFLKKMPKLETSLSHTEEKQDPKKPSCKREGRAPVLLK
 KIQQAEMFPEHSGNVKLSCQFAEIHEDISTICWTKDSSIAQVQRSAGDMSVFAIVQASPKDQGLYYCCIK
 NSYGGKVTAEFNLTAEVILKQLSSRQDTKGCEEIEFSQLIFKEDFLHDSYFGGRLRGQIATEELHFGEVHRK
 AFRSTVMHGLMPVFKPGHACVILKVHNIAIAYGTRNNDELIQRNYKLAAQECYVQNTARYYAKIYAAEAQ
 PLEGFGEVPEIPIFLIHRPENNIPYATVVEELIGEFVKYYSIRDGKEINFLRRESEAGQKCCTFQHWWVYQKTSG
 CLLVTDMQGVGMKLTDVCGIATLAKGYKGFKGNCSMTFIDQFKALHQCNKYCKMLGLKSLQNNNQKQK
 OPSIGSKVQTNSMVTVKKAGPETPGEKKT

Figure 8B

1 atgcggccaga aatccctggat taaaggagta tttgacaaga gagaatgttag cacaatcata
61 cccagctcaa aaaatccctca cagatgtact ccagttatgcc aagtctggccaa gaattttatc
121 aggtgttact gtggccgact gatgtggagac caatgtggaa tagatttttc ctggaccatc
181 tcagctggccaa agggtaaaga aagtgaacaa tggctgttgc aaaagcacac aacgaaaagc
241 ccaacagata cttttggcac gatataatc caagatggag agcacacccca tcatggccaaag
301 tatattagaa cttttatga tacaaaactg gatcatgt tacattttatgttggaaagag
361 tggaaaatgg aactgcccua gcttggatc tcatggccatg ggggcatttca gaactttact
421 atgcccctca aatttaaaga gattttgcgca caagggttgg tttaaagctgc agagacaaca
481 ggagcgtggtaataaactga aggcatcaat acagttgtccaa agcatgttgg ggaatgccttgc
541 aaatcccatt cctcttccatc ctggagaaaa aatggacag tttggaaatccc tcccttgggt
601 gtcatgttgc accagagaga cttttatggaa aatggatgttgg tttgtccatgttgc
661 gataaccccccc tcatggccatc cacaacactc aacagcatgc actggccatc ttttttttttgc
721 gatgtatgggaa ccgtggccaa gatggaaat gaaatgaagc tcatggccaa ctttttttttgc
781 tacctcttc tgcagaaaaat aacttgcgc tcaagacaag gcttggccgtt ctttttttttgc
841 gtgggtggaaag gcttggccaa ctttttttgc tcatggatgttgg agactgttgc
901 ccagttggatgttgg tttgttgggg cacaggttgg gcttggccatc ttttttttttgc
961 cacatggccatc atgaagggat gcttgcgc ttttttttgc ctttttttttgc
1021 cagaacacatc tcaacttttgc ttttttttgc ttttttttgc ttttttttgc
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1321 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1381 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1441 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1501 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1561 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1621 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1681 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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1801 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1861 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1921 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
1981 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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2101 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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2401 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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2521 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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2701 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
2761 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
2821 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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3061 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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3301 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
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3601 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3661 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3721 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3781 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3841 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3901 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc
3961 ttttttttgc ttttttttgc ttttttttgc ttttttttgc ttttttttgc

Figure 9A

Figure 9A

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8041 aagaggcaga gtttgcgtgc ccaatgttcca aactaaagac aicagtttcat tggtcaata
8101 ttgttaccc ttgttaccc ttgttaccc ttgttaccc ttgttaccc ttgttaccc ttgttaccc ttgttaccc

Figure 9A

Human kidney kinase

MSQKSWIKGVFDKRECSTIIPSSKNPHRCTPVCQVCQNLIRCYCGRLIGDHAGIDYSWTIS
 AAKGKESEQWSVEKHTKSPTDTFGTINFQDGEHTHAKYIRTSYDTKLDHLLHLMLKE
 WKMEPLKLVISVHGGIQNFTMPSKFKEIFSQGLVKAETTGAWIITEGINTVSKHVGDAL
 KSHSSHSLRKIWTVGIPPWGVENQRDLIGKDVVCLYQTLDNPLSKLTLNSMHSHFILS
 DDGTVGKYGNEMKLRRNLEKYLQLQKIHCRSRQGVVGLVVEGGPNVILSVWETVKD
 KDPVVVCEGTGRAADLLAFTHKHLAEGMLRPQVKEEICMIQNTFNFSLKQSKHLFQIL
 MECMVHRDCITIFDADSEEQQDLDLAILTALLKGTNLSASEQLNLAMA WDRVDIACKHI
 LIYEQHWKPDALEQAMSDAL VMDRVDFVKLLIEYGVNLHRLTIPRLEEL YNTKQGPTN
 TLLHHLVQDVVKQHTLLSGYRITLIDIGLVVEYLIGRAYRSNYTRKHFRAL YNNLYRKYK
 HQRHSSGNRNESAESTLHSQFIRTAQPYKFKEKSIVLHKSRRKSKEQNVSDPESGFLY
 PYNDLLVVAVLMKRQKMAMFFWQHGEATVKA VIACIL YRAMAHEAKESHMVDDAS
 EELKNYSKQFGQLALDLLEKAFKQNERMAMTLLTYELRNWSNSTCLKLA VSGGLRPFV
 SHTCTQMLLTDMWMGRLKMRKNSWLKIIISIILPPTILTLEFKSKAEMSHVPQSQDFQFM
 WYYSDQNASSSKESASVKEYDLERGHDEKLDENQHFGLESGHQHLPWTRKVYEFYSAP
 IVKFWFYTMA YLAFLMLFTYTVL VEMQPQPSVQEVL VSIYIFTNAIEVVREVSISEPGKF
 TQKVKVWWISEYWL TETVAIGLFSAGFVLRWGDPPHTAGRLIYCIDIIFWFSRLLDFFA
 VNQHAGPYVTMIAKMTA NMFYIVIMAI VLLSGFVARKA ILSPKEPPSWSLARDIVFEPY
 WMIYGEVYAGEIDVCSSQPSCPPGSFLTPFLQAVYLFVQYIIMVNLLIAFFNNVYLDMESI
 SNNLWKYNRYRYIMTYHEKPWLPPPLILLSHVGLLRRRLCCHRAPHDQEEGDVGLKLY
 LSKEDLKKLHDSEEQCVEKYFHEKMEDVNCSCERIRVTSERVTEMYFQLKEMNEKVS
 FIKDSLLSLDSQVGHQLQDLSALTVDLKVL SAVDTLQEDEALLAKRKHSTCKKLPHSWS
 NVICAEVLGSMEIAGEKKYQYYMPSSLLRSLAGGRHPPRVQRGALLEITNSKREATNV
 RNDQERQETQSSIVVSGVSPNRQAHSKYGQFLVPSNLKRVFSAETVPLSRPSVPDVL
 ATEQDIQTEVLVHLTQTPVVS DWASVDEPKEKHEPIAHLLDGQDKAEQVLPTLSCTPE
 PMTMSSPLSQAKIMQTGGGYVNWAFSEGDETGVFSIKKKWQTCLPSTCDSDSSRSEQHQ
 KQAQDSSLSDNSTRSAQSSECSEVGPWLQPNTSFWINPLRRYRPFARSHSFRHKEEKL
 KICKIKNLGSSEIGQGAWVKAKMLTKDRRLSKKKNTQGLQVPIITVNACSQSDQLNP
 EPGENSISEEEYSKNWFTVSKFSHTGVEPYIHQKMKTKEIGQCAIQISDYLKQSQEDLSKN
 SLWNSRSTNLNRNSLLKSSIGVDKISASLKSPQEPHHYSAIERNNLMRLSQTIPFTPVQL
 FAGEEITVYRLEESSPLNLDKSMSSWSQRGRAAMIQVLSREEMDGLRKAMRVVSTWS
 EDDILKPGQVFIVKSFLPEVVRTWHKIFQESTVLHLCLREIQQQRAAQKLIYTFNQVKPQ
 TIPYTPRFLEVFLIYCHSANQWL TIEKYMGEFRKYNNNNGDEITPTNTLEELMLAFSHW
 TYEYTRGELLVLDLQGVGENLTDPsvIKPEVKQSRGMVFGPANLGEDAIRNFIAKHHCN
 SCCRKLKLPDLKRNDYS PERINSTF GLEIKIESAEEPPARETGRNSPEDDMQL

Figure 9B

Figure 10A

Figure 10A

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MEVAWL VYVLGQQPLARQGEQGSRL VPGRGL VLWLPGLPRSSPSWPAVVDLAPARPRGLPLICHTGHEQAGREPGPGSST
KGPVLHDQDTRC AFLPRPPGPLQTRR YCRH QGRQGSGLGAGPGAGT WAP APPGVSKPRCPGRARPGEGQQVTTARPPAIN
RGARQPRAGAAAAGRGGAGAWRTGEAAASAGPAVGEggAMGSSRRAPTRGWGAGGRSGAGGDGEDDDGPVWIPSPASRS
YLLSVRPETSLSSNRLSHIPSSGRSTFCIIAQQLTEETQPLFETTLKSRSVSEDSDVRFCTCIVTGYPEPEVTVYKDDTELDRYCGL
PKYEITHQGNRHTLQLYRCREEDAIIYQASAQNSKGIVSCSGVLEVGTMTEYKIHQRWFAKLKRKA AAKLREIEQSWKHEK
AVPGEVDTLRLSPDRFQKRRLSGAQAPGPSVPTREPEGGTLAAWQEGETETAQHSGLGLINSFASGEVTTNGEAAPENGE
DGEHGLLTYICDAMELGPQQRALKKEESGAKKKDEESKQGLRKPELEKA AQSRRSSEN CIPSSDEPDSCGTQGPVGVQEQQVT
QPRGRGAAARGPGSSGTDSRKPA SAVGTPDKA A QKAPGPQEVYFSLKDMYLEN TQAVRPLGEEGPQTLSVRAPGESPKGK
APLRARSEGVPGAPGQPTHSLTPQPTRFNKRFAPKPKGEATTDSKPISSLSQAPECGAQSLGKAPPQASVQVPTPPARRH
GTRDSTLQGQAGHRTPGEVLECQTTTAPTM SASSSDVASIGVSTSGSQGIIEPMDMETQEDGIRTSANQRTGSKKNVQADGK
IQVDGRTRGDGTTQTAQRTRADRKQTQVDA GTQESKRPQSDRSAQKGMMTQGRAETQLETTQAGEKIQEDRKAQADKGTQE
DRRMQGEKGMMQGEKGTQSEGSAQMEGQSEQEVATSLGPSSRTPKLPPTAGPRAPLNIECFVQTPEGSCKFPKKPGCLPRSEE
AVVTASRNHEQTVLGPLSGNLMMLPAQPPHEGSVEQVGGGERCRGPQSSGPVEAKQEDSPFQCPKEERPGGVPCMDQGGCPLA
GLSQEVPTMPSLPGTGLTASPKAGPCSTPTSQHGSTATFLPSEDQVLMSSAPTLHILGLGTPPTQSHPPETMATSSEGACAQVPD
VEGRTPGPRTSCDPGLIDSLKNYLLLKLSSSETSGAGGESQVGAATGGGLVPSATLTPTVEVAGLSPRTSRRILVERVENNHLV
QSAQQTLLSPCTSRRLTGLLDREVQAGRQALA AARGSWGPGPSSLTVPAIVVDEEDDPGLASEGASEGEGEVSL
QESSMAGRILGEAGGQAAAPGQQGPSAESIAQEPSQEKEKFPGEALTGTPAATPEELALGARRKRFLPKVRAAGDGEATTPPEERES
PTVSPRGPRKSLVPGSPGTPGRERRSP TQGRKASMLEV PRAEEELAAGD LGPSPKAGGLDTEVALDEGKQETLAKPRKA KDL
LKAPQVIRKIRVEQFPDASGSLKLWCQFFNILSDSVLTWAKDQRPVGEVGRSAGDEGPAALAI VQASPVD CGVYRCTIHN
GSASTDFCLSPEVLSGFISREEGEVGEIEMTPMVFAKGLADSGCWGDKLFGRLVSEELRGGGYGCGLRKASQAKVIVYGLEPI
FESGRTCIUKVSSLLVFGPSSSETSLVGRNYDVTIQQGCKIQNMSREYCKI AAEARAAPGFGEVPEIPLYLIYR PANNIPYATL
DLGKPLLESYCSREWGC AEA PTA SGSSSEAMQKCQTFQH WLYQWTNGSFLVTDLAGVDWKMTDVQIATKLRGYQGLKESCF
PALLDRFASSHQCNAYCELLGLTPLKGPEAHPQAKGSKSPSAGRKGSQLSPQPKKGLPSAPSSKATPQASEP
VTTQLLGQQPPTQEEGSKAQGMR

Figure 10B

Figure 11A

MNNQKVVAVLLOECKQVLDQQLLEAPDVSEEDKSEDQRCRALLPSELRTLQEAKEMKWPFVPEKWQY
 KQAVGPEDKTNLKDVGAGLQQLLASLRASILARDCAAAAVFLVDRFLYGLDVSGKLLQVAKGLHKL
 QPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNNGATGTWLYRNESDKVLVQSVCIQIRGQILQKLGM
 WYEAAELIWAISIVGYLALPQPDKKGLSTSLGILADIFVSMSSKNDYEKFKNNPQINLSSLKEFDHHILSAA
 ACKLAAAFSAYTPLFVLTAVNIRGTCLLSSNDCPPPELKNLHLCEAKEAFEIGLLTKRDEPVTGKQEL
 HSFVKAAFGLTTVHRRLLHGETGTVHAASSQLCKEAMGKLÝNFSTSSRSQDREALSQEVMSVIAQVKEHLQ
 VQSFNSNVDDRSYVPESECRLDKLILHGQGDFQKILDTRYSQHHTSVCEVFESDCGNNKNEQKDAKTVGCVI
 TALKTEIKNIDTVSTTQEKKPHCQRDTGIISSSLMGKNNVQRELRRGRRNWTHSDAFRVSLDQDVETETEPSD
 YSNCEGAVFNKSLSGSQTSSAWSNLSGFSSSASWEEVNYHVDDRSARKKEPGKEHLVDTQCSTALSEELEN
 DREGRAMHSLHSQQLHDLSLQEPNNNDNLEPSQNNQPMPLTPFSPHNTPGIFLAPGAGILLEGAPEGIQEVR
 NMGPRNTSAHSRPSYRSASWSSDSGRPKNMGTQPSVQKEEAFEIIVEFPETNCVDVKDRQGKEQGEISERG
 AGPTFKASPSWVDPGETAESTEDAPLDFFHRVLHNSLGNISMILPCSSSFTPNWPVQNPDSRKSGGPVAEQGI
 DPDASTVDEEGQLLDSMDVPCNNGHGSHRLCILRQPPGQRAETPNSSVSGNILFPVLSEDCTTEEGNQPG
 NMLNCQNSSSSVWWWLKSPAFTSSGSSWVSLPGKMRKEILEARTLQPDDEKLLA
 GVRHDWLFQRLENTGVFKPSQLHRAHSALLKYSKSELWTAQETIVYLGDYLTVKKGRQRNAFWVH
 HLHQEEILGRYVGKDYKEQKGLWWHFTDVERQMTAQHYYTEFNKRLYEQNIPTQIFYIPSTILLIEDKTK
 GCISVEPYILGEFVKLSNNNTKVVKTEYKATEYGLAYGHFSYEFSNHRDVVVDLQGWVVTGNGKGLIYLTD
 QIHSVDQKVFTTNFGKRGIFYFFNNQHVECNEICHRLSSLTRPSMEKP

Figure 11B

FIGURE 12

HeEF-2_kinase>
MHCK_B>
Melanoma_kinase>
Kidney_kinase>
Muscle_kinase>
Heart_kinase>
Lymphocyte_kinase>
consensus

1 EED--SGLICAGAOPFGRL--RSCSTKIGSNP--WKGASH--WRRHIEPDR--DVW
1 ECT--ATLQGEPVPPFAE--PPTLTDIS--KSGASGRS--SIGKKPTPR--PSHP
1 EQLGLCAKQEPFLQDENG--QTRVWQCTWS--EDDQLKSHLQ--SELPEVNTWSSIDQ--TVLHICLRE
1 SQRGRAAMQQLRQEMD--WVSVVSTWS--EDDQLKQVQVW--SELPEVRTWKKISQ--STVLHICLRE
1 GDK--WPGRVVQLRGCGYCC--SOAKVSYG--LEPPFRSRTCQ--VSSLLVGPSSSETSLVGRNMYDFTIQG
1 EGGR--WPGQSAEELHF--BGVH--ESTWHDG--LMPWPKFHAC--VHNAIAYGTRNNDELQQRNYRQAAQE
1 EAGSTIYGDYLTVKXX--EQNENVHHH--QEEILGRGQDQKQKGL--WHRFT
1 wt v im se G amRkafr 1 i g yvik y v y ed 1

HeEF-2_kinase>
MHCK_B>
Melanoma_kinase>
Kidney_kinase>
Muscle_kinase>
Heart_kinase>
Lymphocyte_kinase>
consensus

62 WRLMMEVLAQESTRHLWPKQ--WVIMQSCIMEKQD-P-GKPLSH--WVIMQSCIMEKQD-P-GKPLSH--PDRDN-IR
56 EKQAMIKRSMADIKPSF--PKK--IEFLQSCVIEPFDQT-SSDLICG-A-P-MD-VGRVQVSS--PDRDN-IR
74 EOCGRACQLTPAQMIKSI--PYSRPFEMTLYCH-SAGQPA-V-ECHT--VGRVQVSS--PDRDN-IR
74 EOCGRACQLIYTQVQVOTI--PYTRPFEVETYCH-SAGQPA-V-ECHT--VGRVQVSS--PDRDN-IR
75 CTKENMSEEVCKIAAAEARAAPGPGEV--ECPHPEVY-PANNIPIAT--EDGKPLS-CSRENGCAEAPTAGSSEAM
73 CYVNTTYYEAKIAAAEARAAPGPGEV--ECPHPEVY-PANNIPIAT--EDGKPLS-CSRENGCAEAPTAGSSEAM
58 VERTMTQHEVTE--KRLYEQNIPTQFYPSTI--ILEDKTIKGCI--PEL--VLS--TK--WVKTSEYKAT
81 v iQ akkw fu kp dip al iflv r f 18 yi gef kynn g v dt

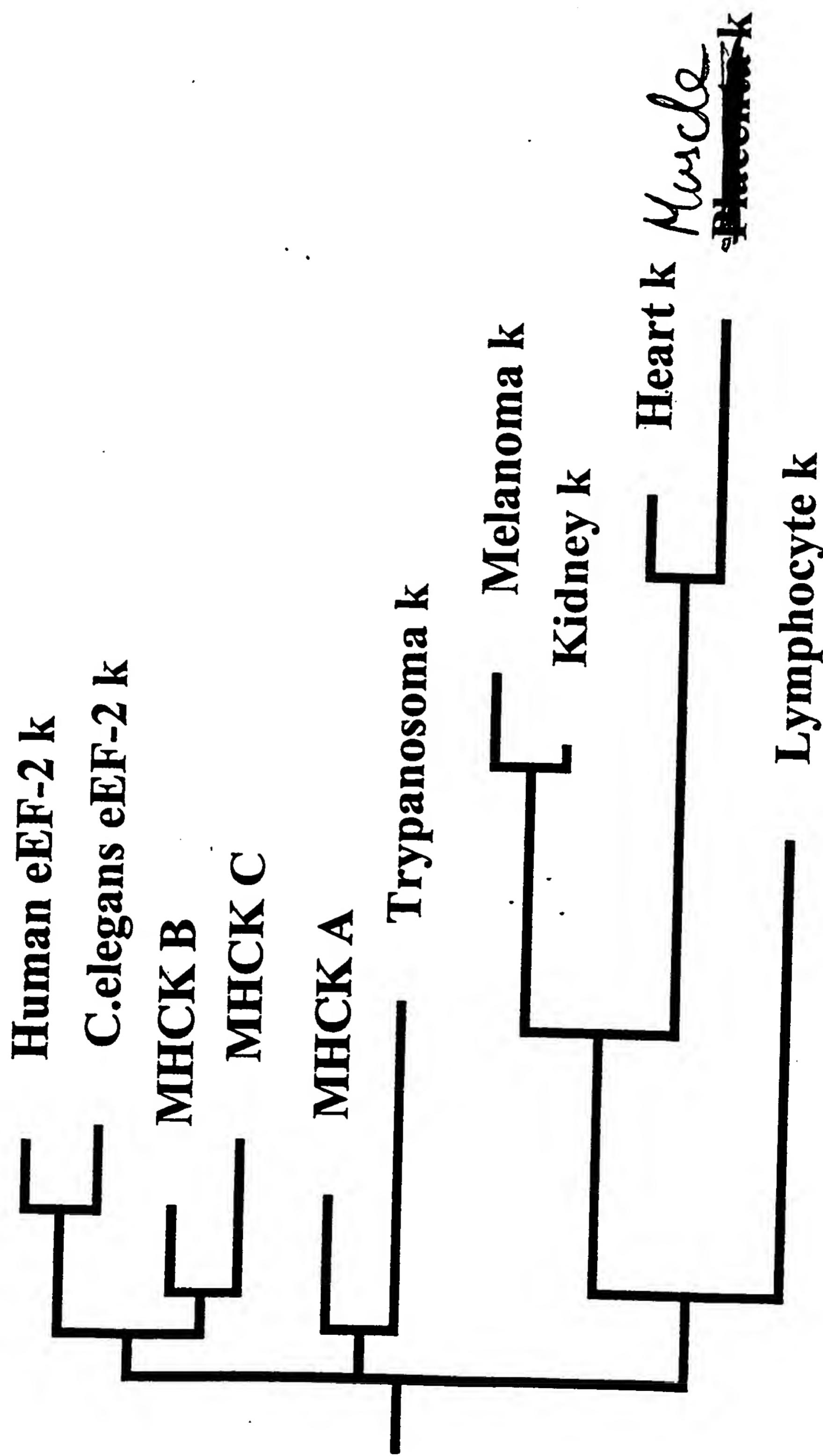
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Melanoma_kinase>
Kidney_kinase>
Muscle_kinase>
Heart_kinase>
Lymphocyte_kinase>
consensus

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124 NTPQMLVH--F-RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
145 EIMLMLPQ--F--RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
145 EIMLMLPQ--F--RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
154 QKCCTQO--L--F--RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
150 QKCCTQO--V--F--RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
132 SYGL--E--F--F--RSGHQF--M--ELYKQVQHET--TD--DQ--VR--EALAPYS--AERI
161 afshwtyeyt g llvvDlqG vg d 1TDpqi t d g fg gnlg gm F H CN C

HeEF-2_kinase>
MHCK_B>
Melanoma_kinase>
Kidney_kinase>
Muscle_kinase>
Heart_kinase>
Lymphocyte_kinase>
consensus

196 ESEGAPP
190 QYIQS
216 EKQKPD
216 EKQKPD
221 ELCGTP
217 ESGGKSH
206 ERSSTRP
241 r l L i

PHYLOGENETIC TREE OF ALPHA-KINASES



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FIGURE 13

FIGURE 14

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601-1-098C1

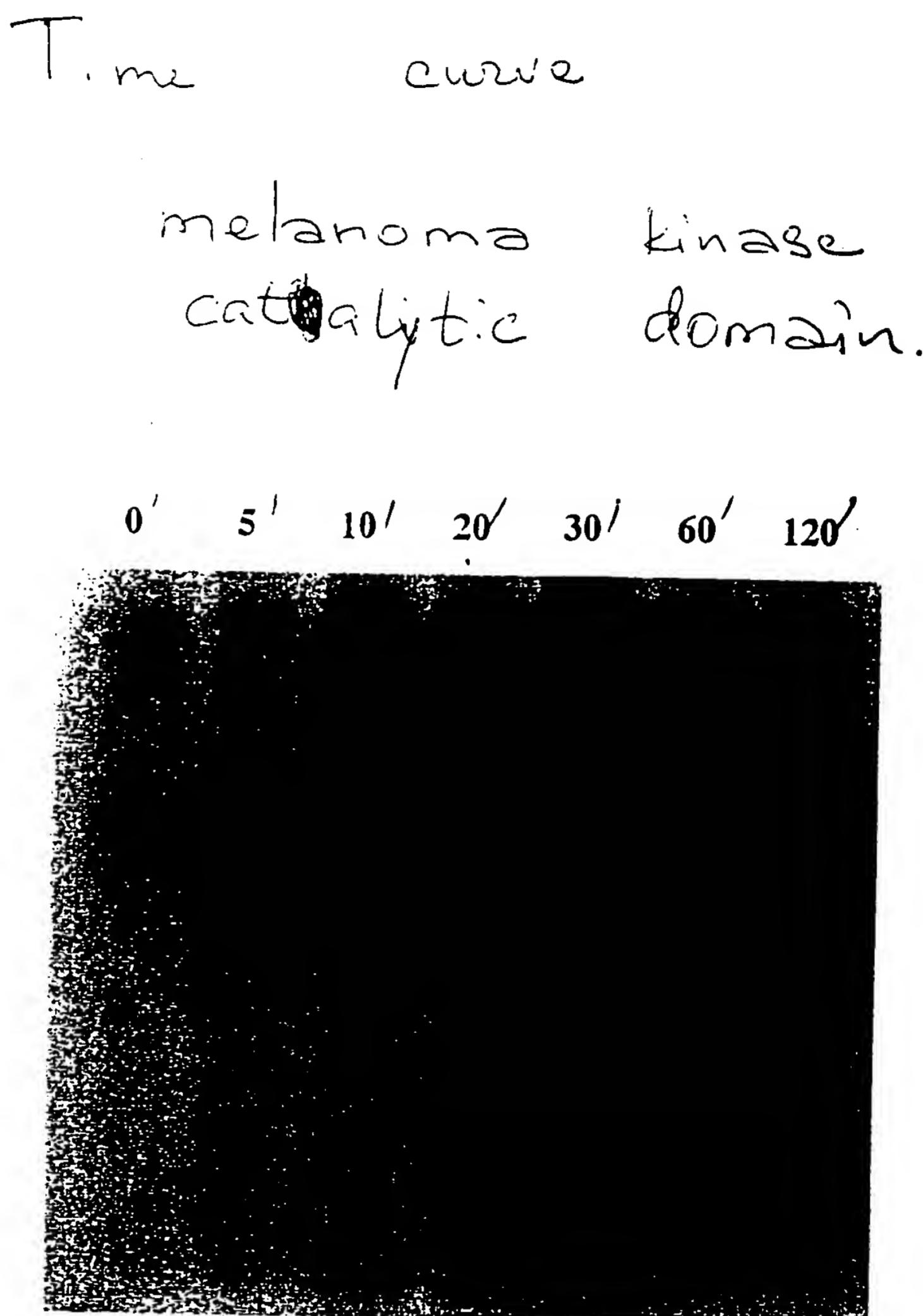
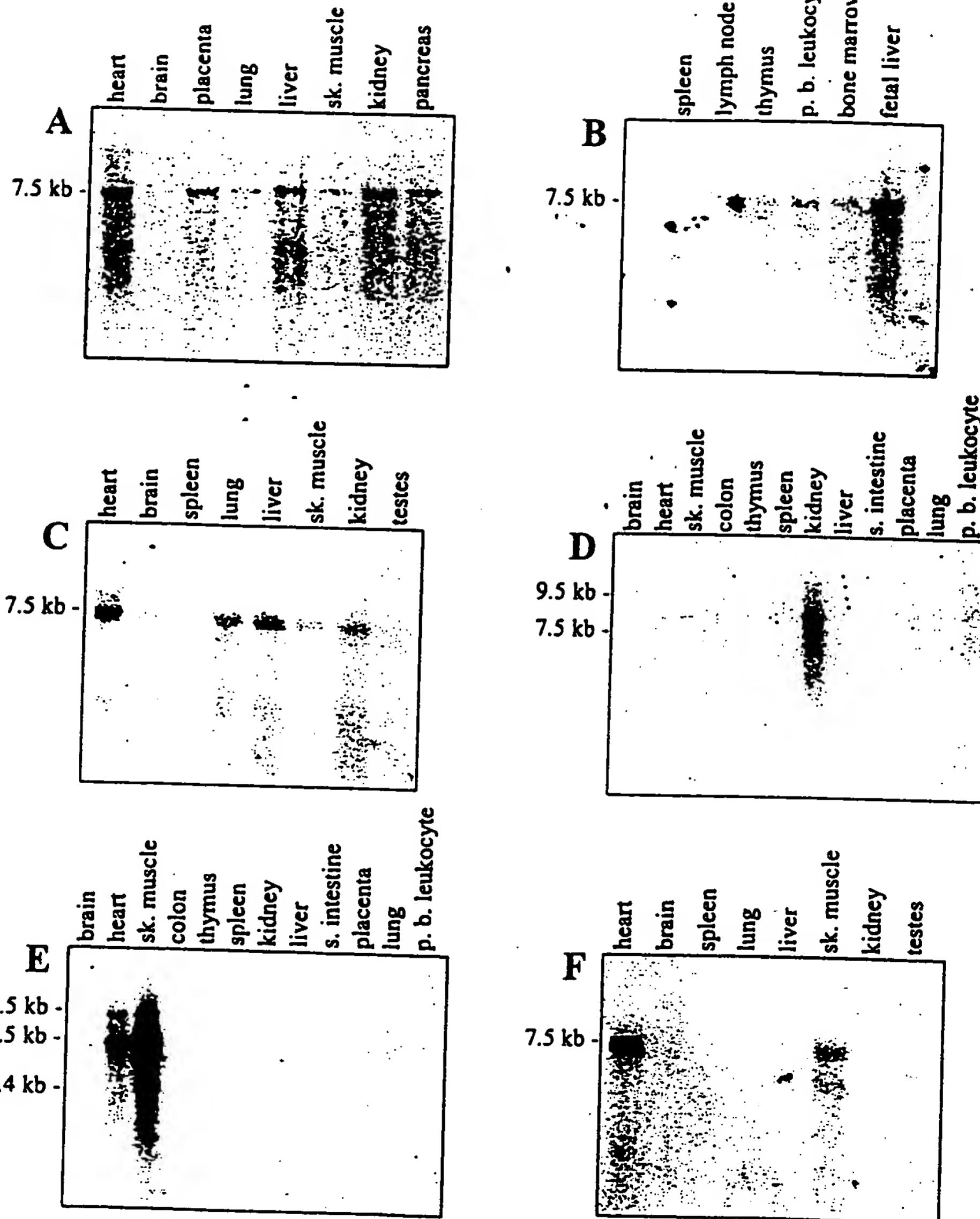


FIGURE 15

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01-1-098 CP



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 ME> 1

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 ME> 1

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 MK> 131 ANHVGDAALI
 KK> 131 ANHVGDAALI
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 ME> 473 1CL1PDKK1EL1NVA

 MK> 513 NNRRSGRATSSST
 KK> 513 -R
 ME> 494

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 ME> 743 1CL1PDKK1EL1NVA

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 ME> 808 1CL1PDKK1EL1NVA

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 MK> 1023 1CL1PDKK1EL1NVA
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 ME> 919 1CL1PDKK1EL1NVA

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 KK> 1033 1CL1PDKK1EL1NVA
 ME> 979 1CL1PDKK1EL1NVA

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 KK> 1093 1CL1PDKK1EL1NVA
 ME> 1039 1CL1PDKK1EL1NVA

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 ME> 1310 1CL1PDKK1EL1NVA

 MK> 1544 1CL1PDKK1EL1NVA
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 ME> 1316 1CL1PDKK1EL1NVA

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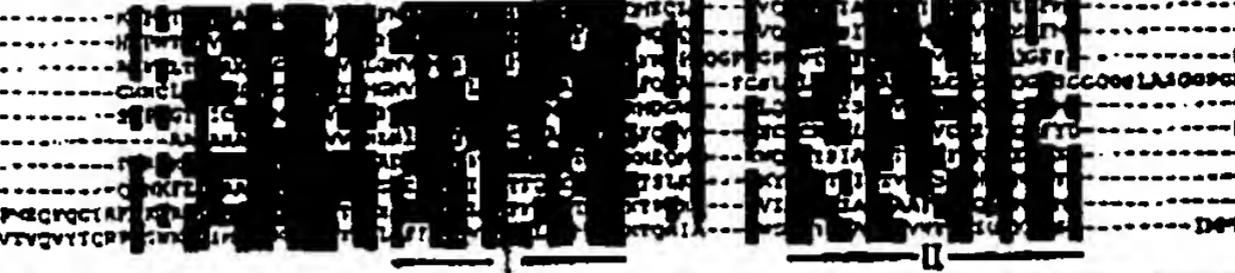
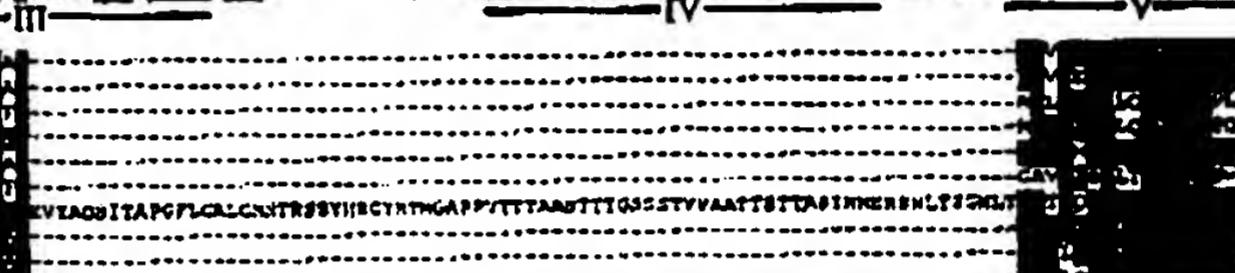
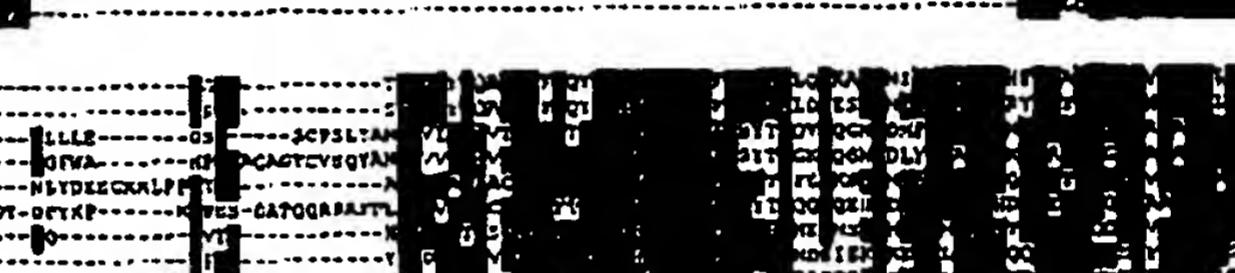
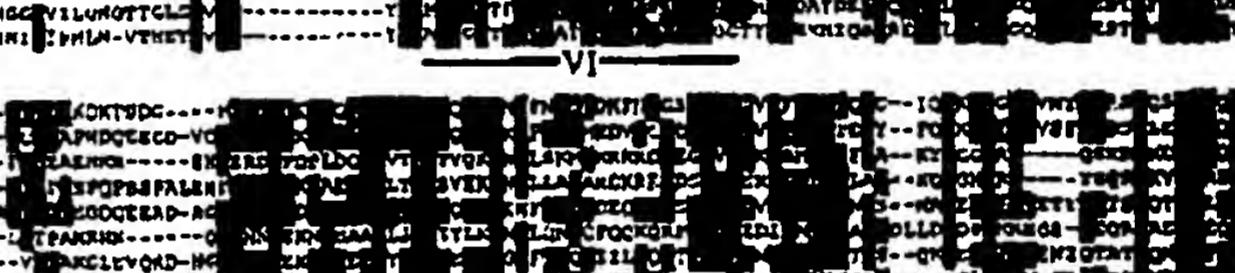
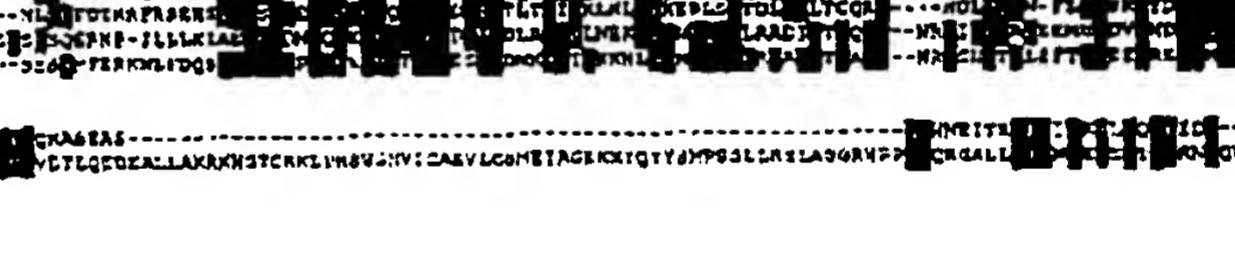
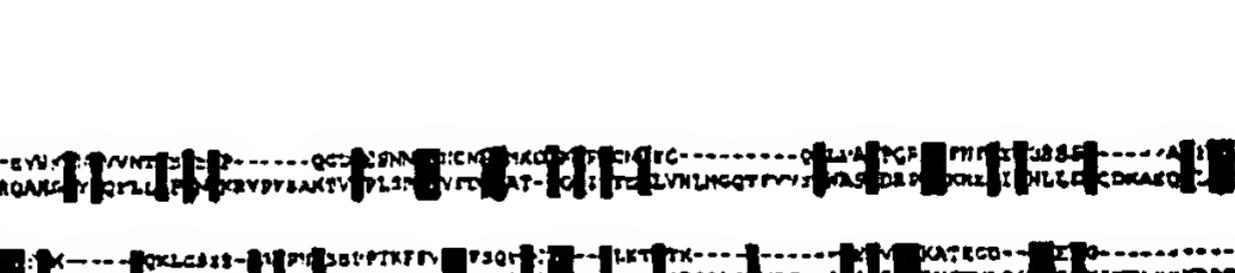
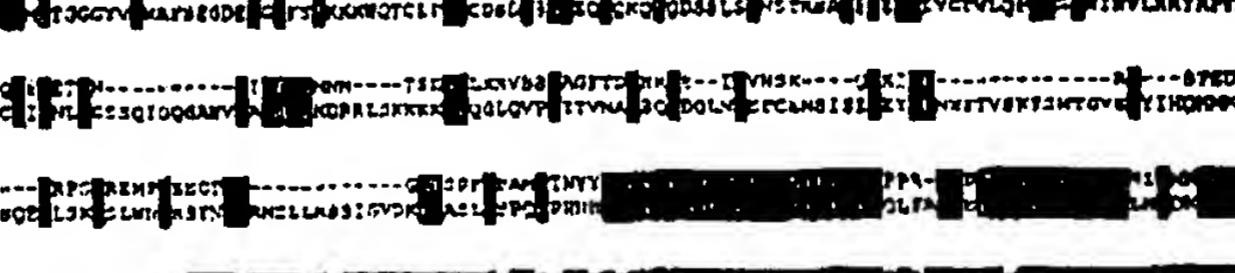
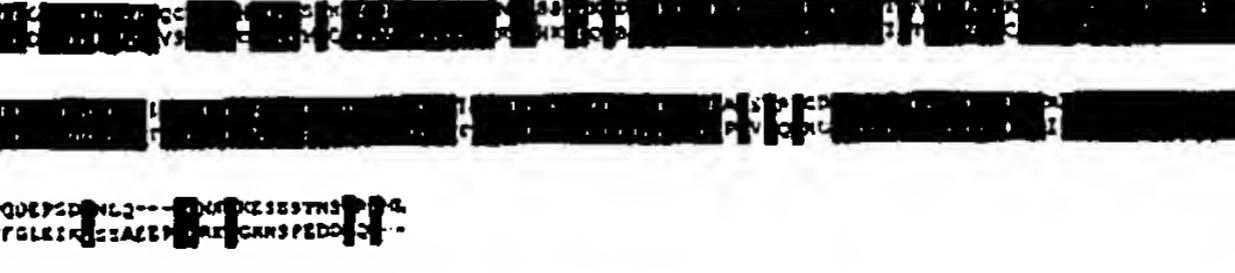
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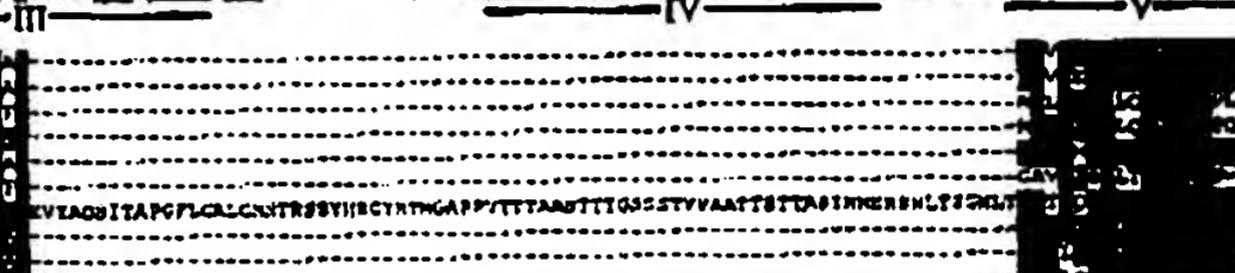
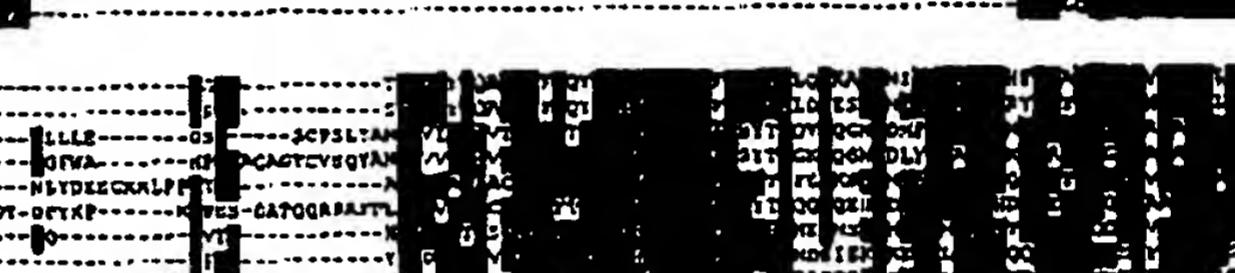
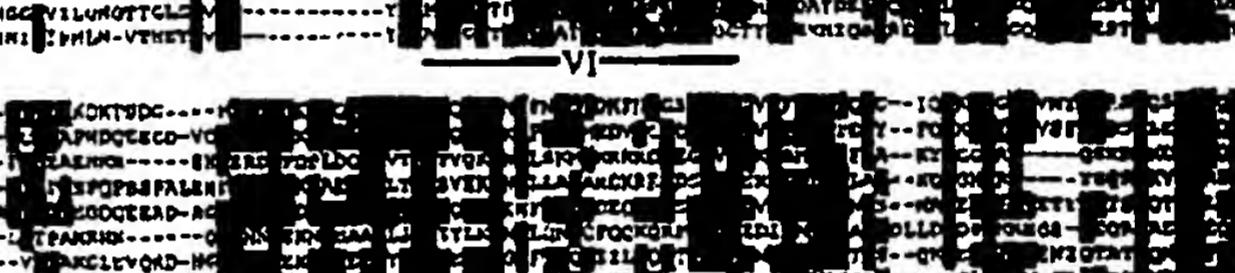
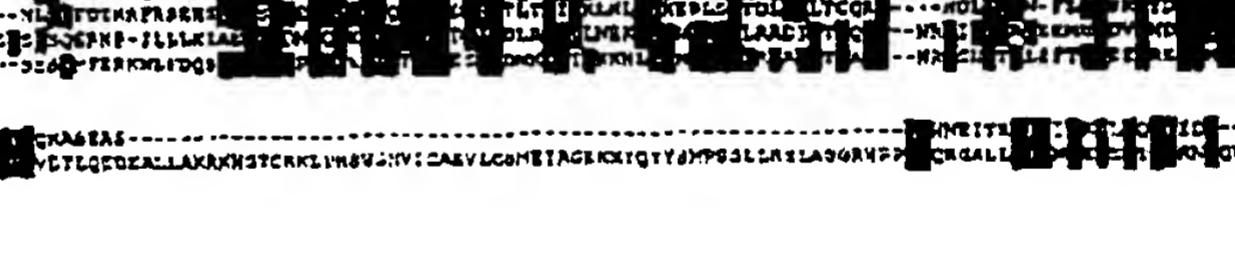
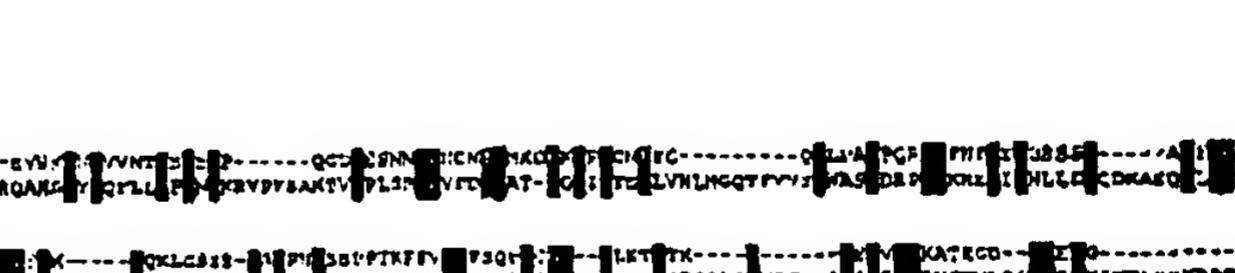
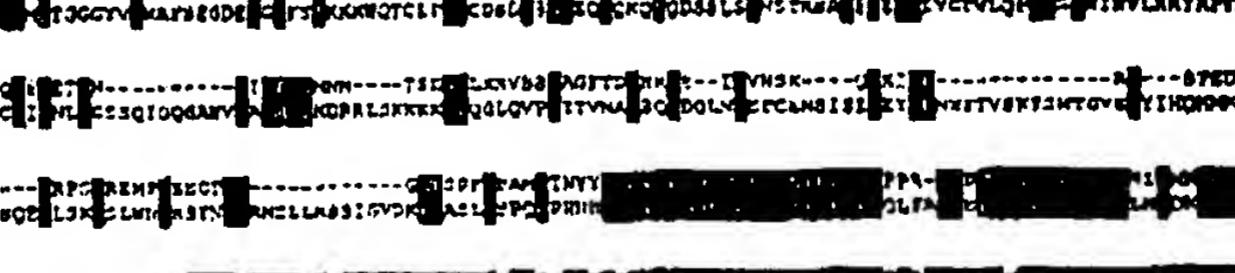
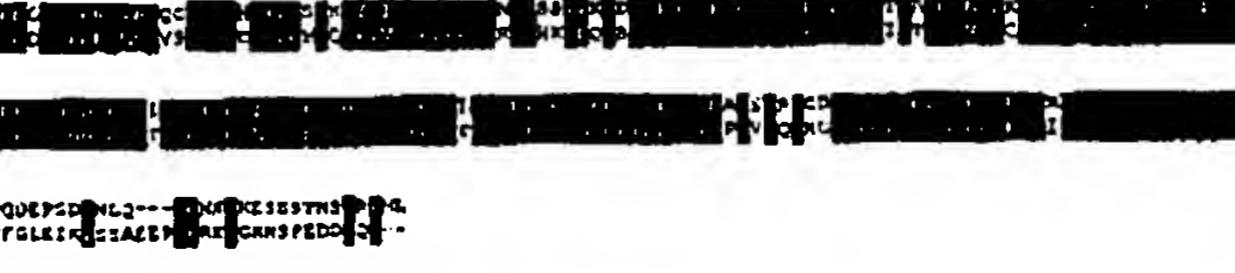
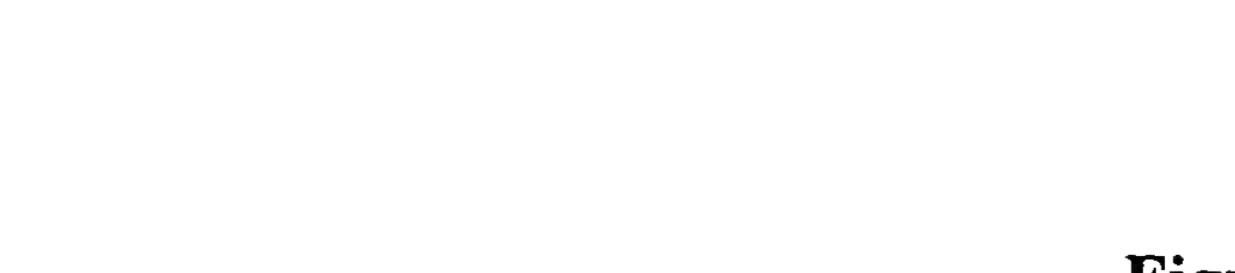
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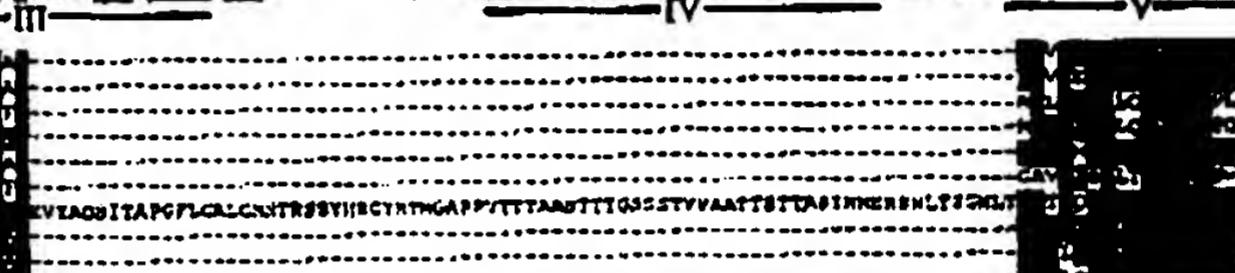
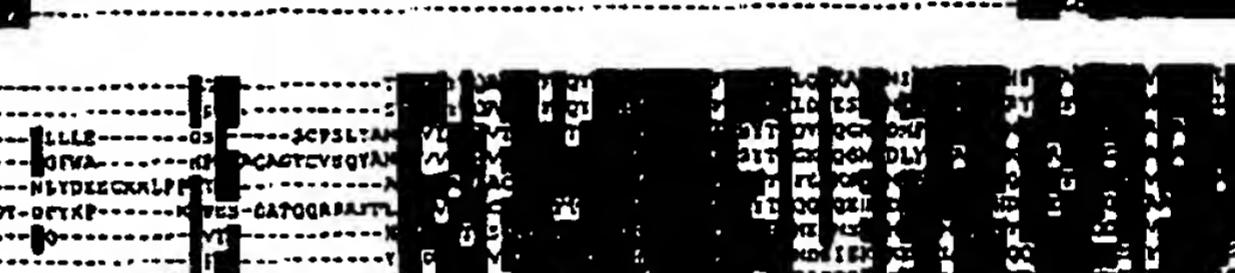
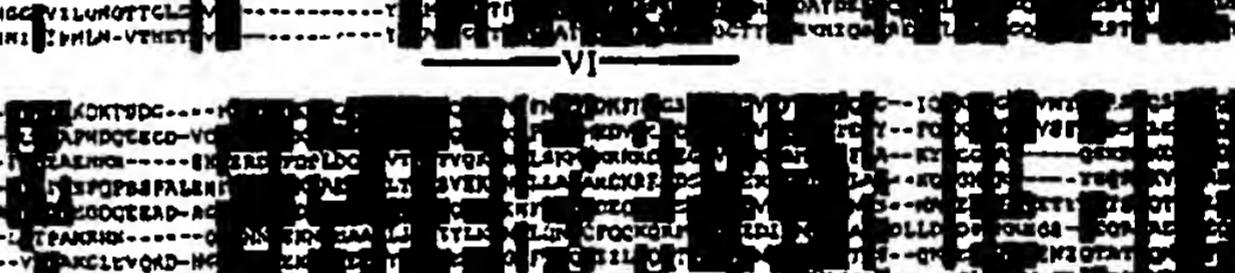
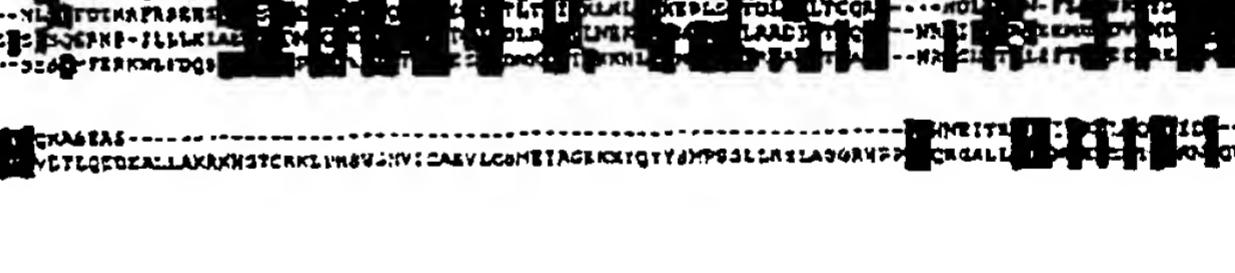
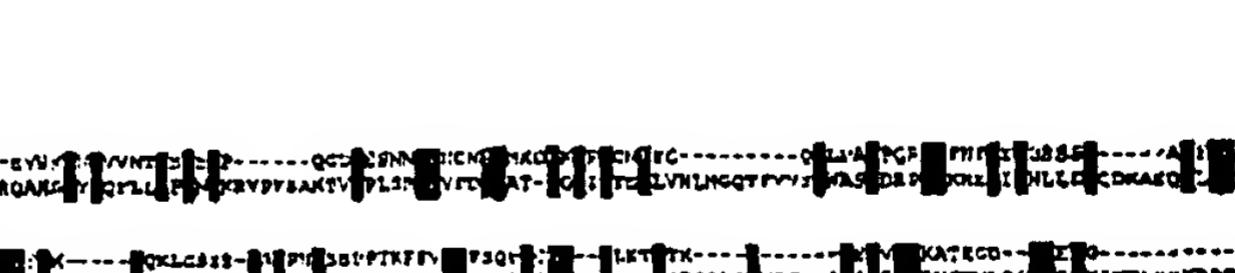
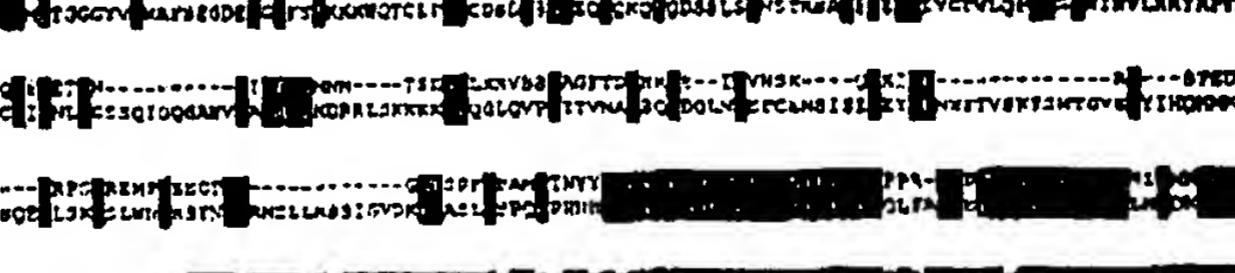
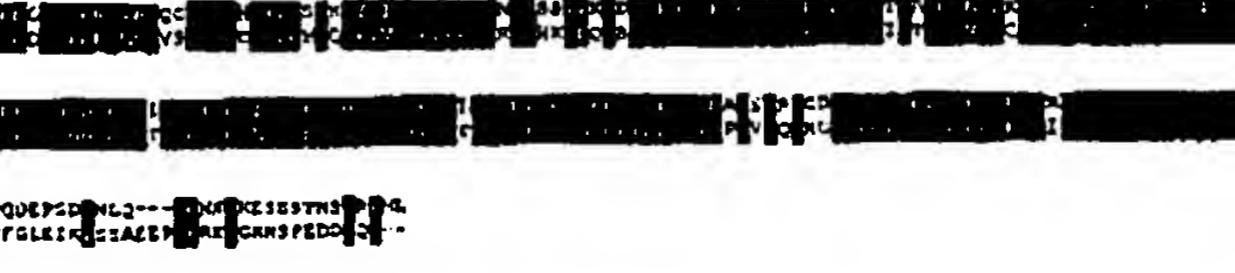
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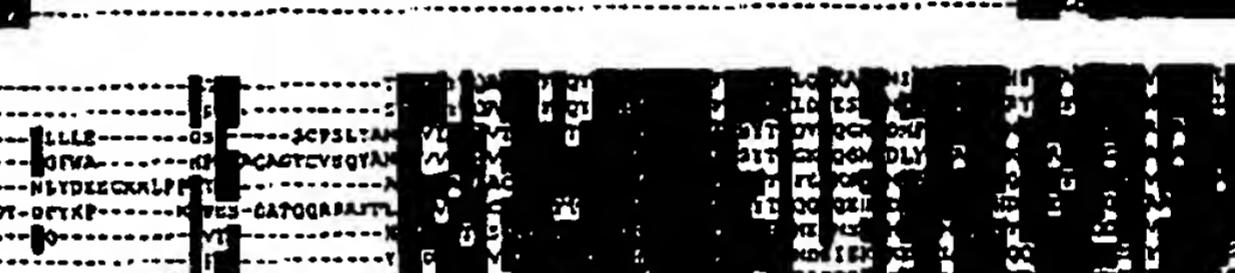
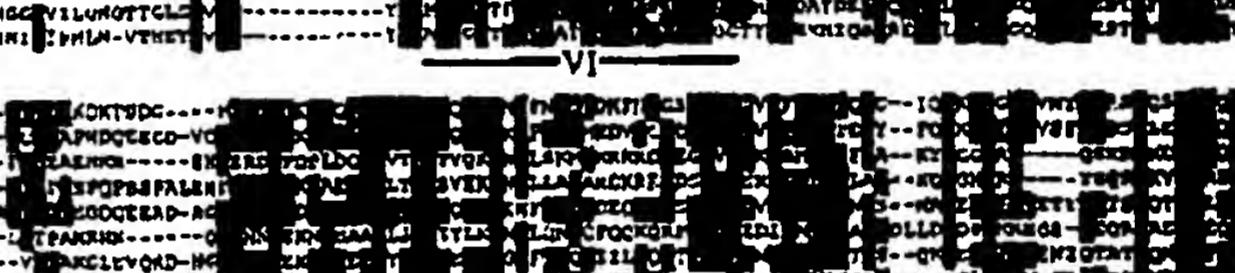
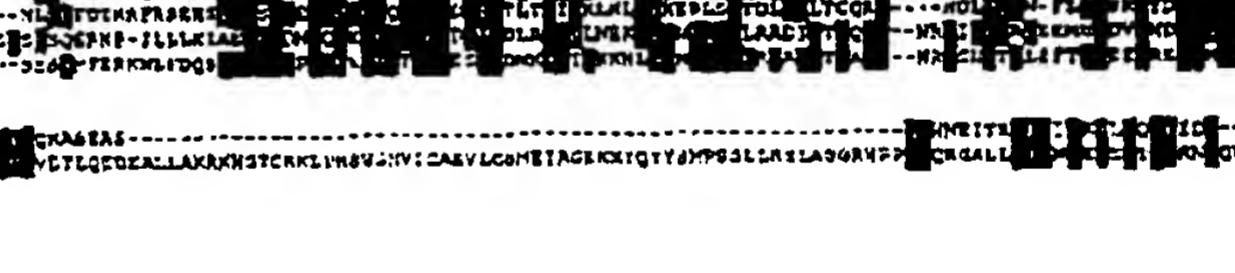
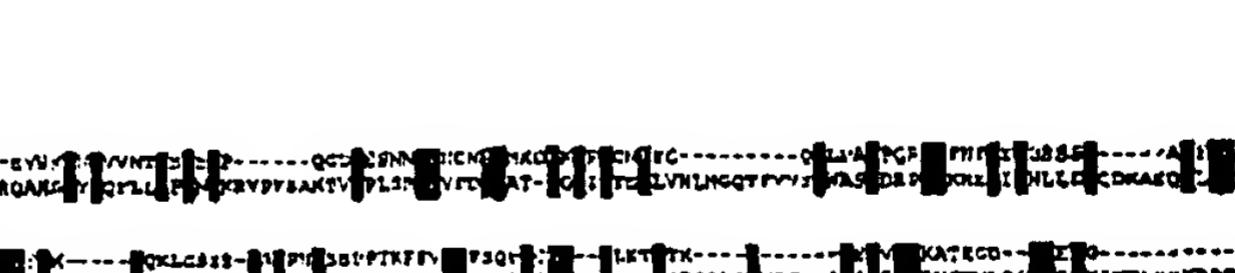
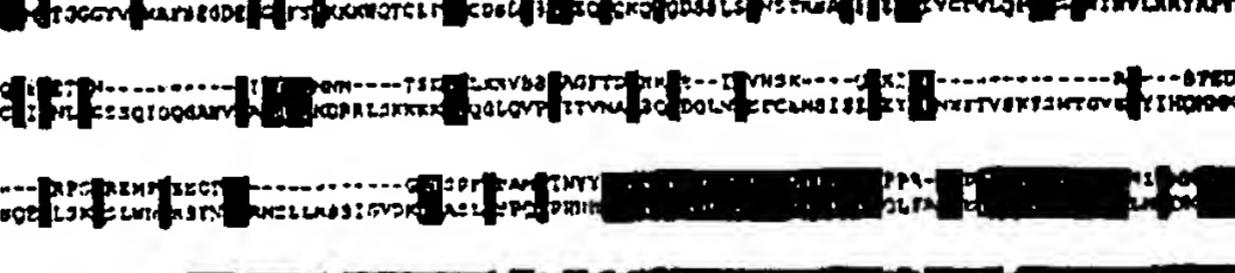
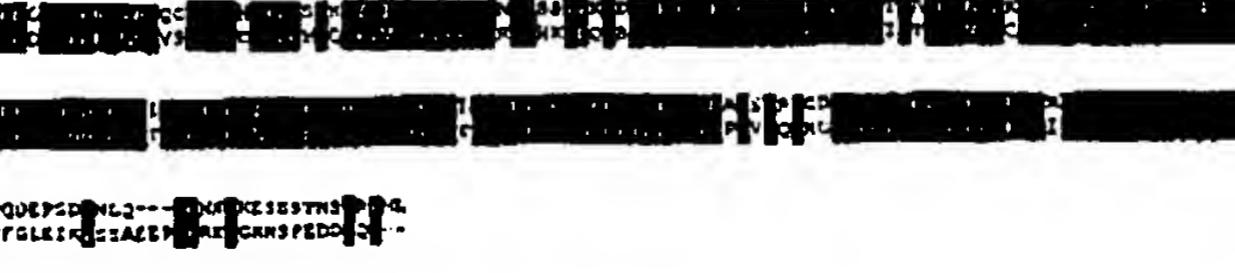
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 KK> 1990 1CL1PDKK1EL1NVA
 ME>

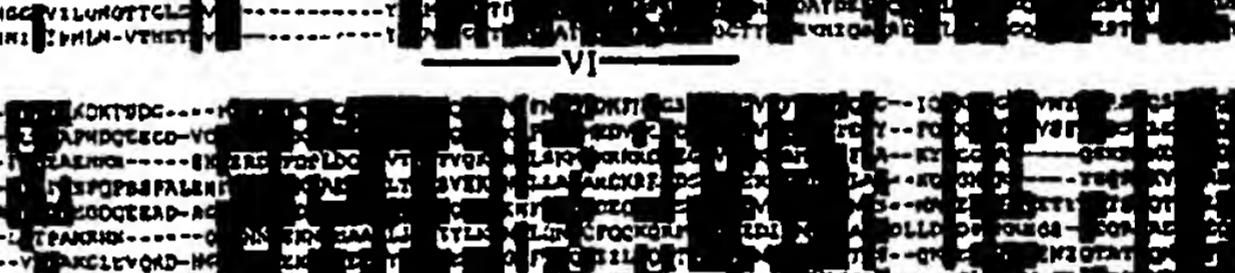
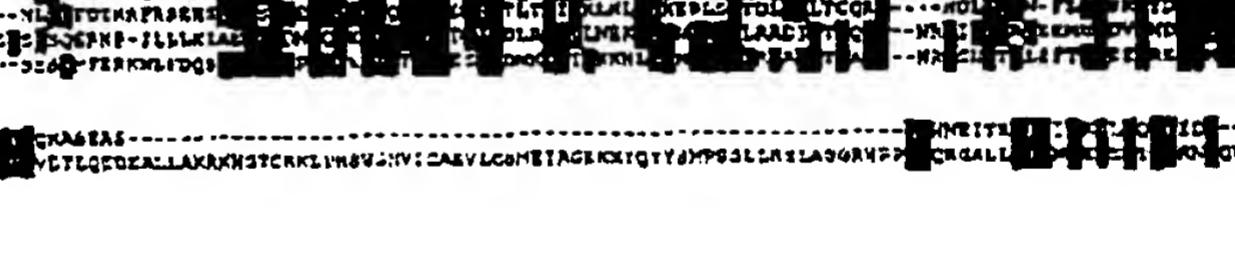
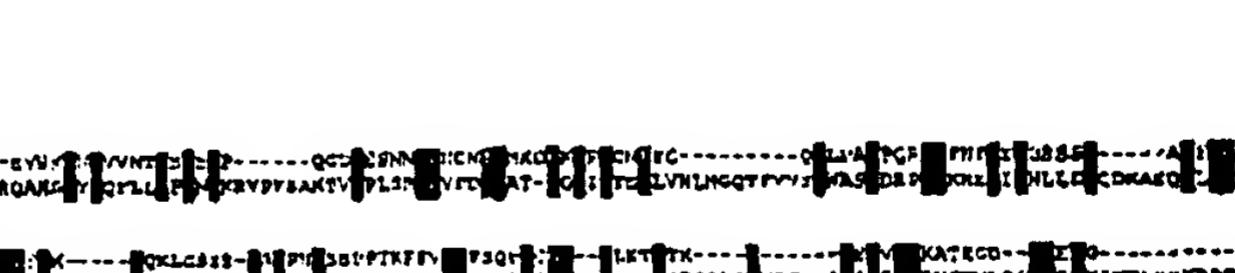
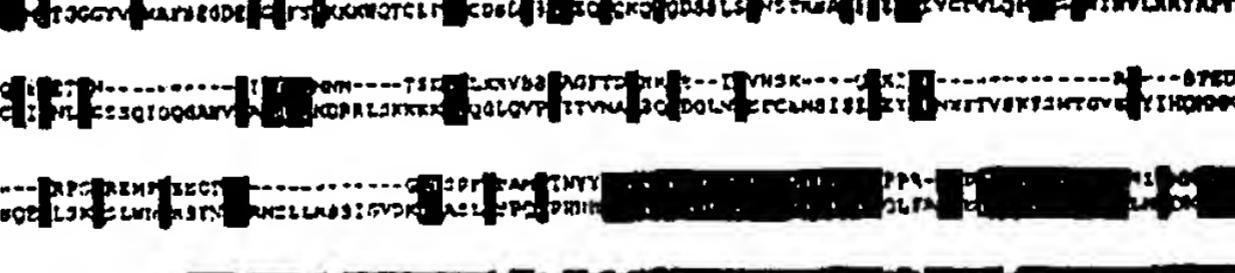
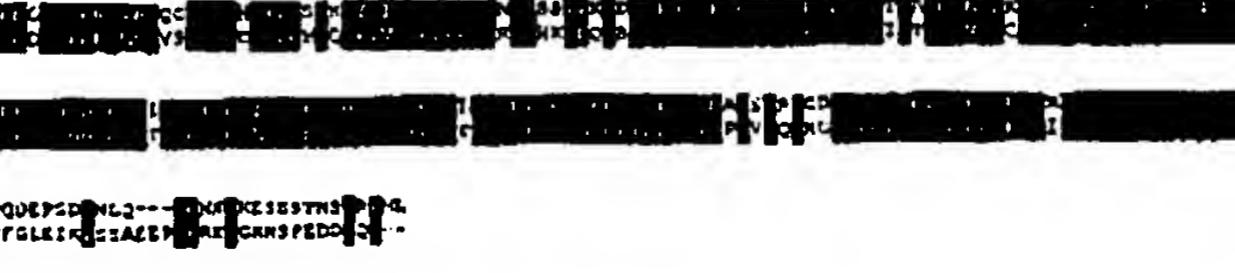
Figure 17

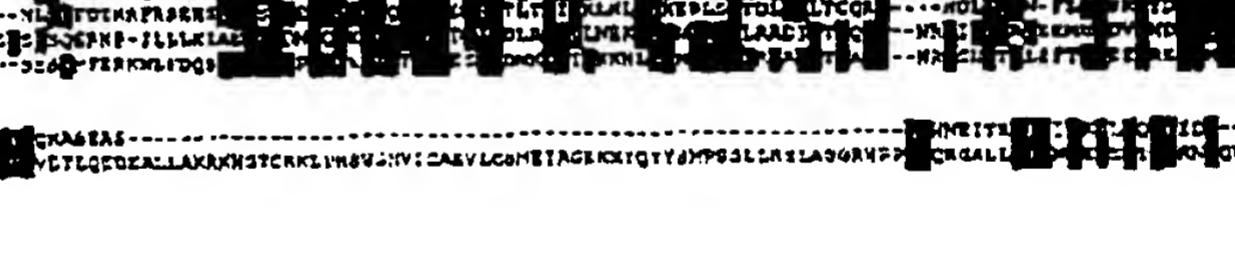
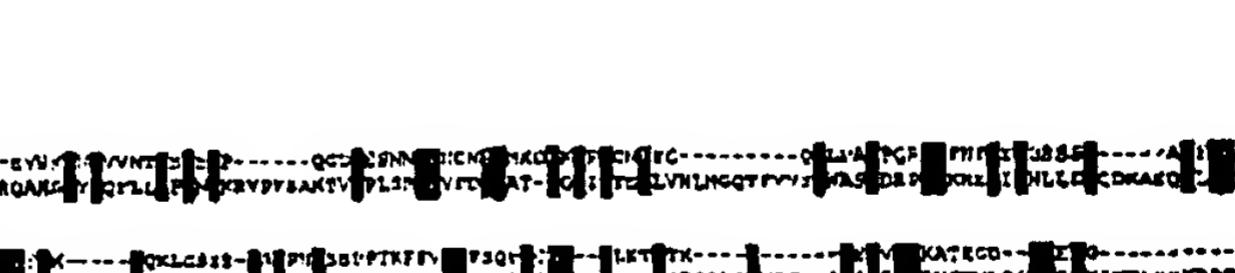
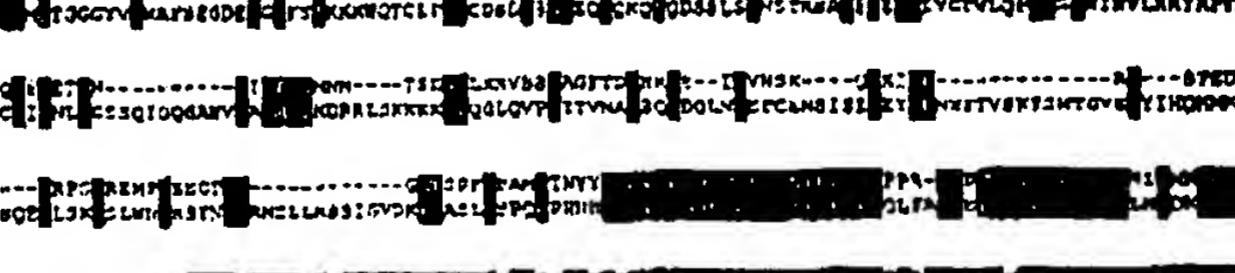
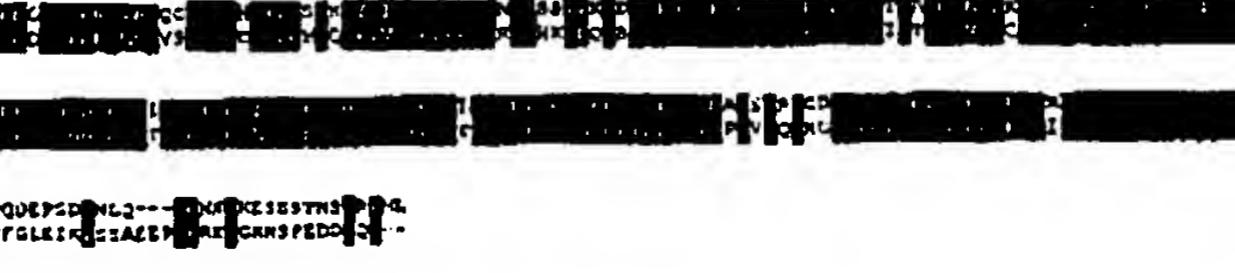
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 KIDNEY_KINASE> 602 
 LTRPC1_MTR1> 717 
 LTRPC2> 591 
 MELASTATIN> 742 
 LTRPC1_TRPC1> 733 
 DMLTRPC> 810 
 COLTRPC> 876 
 COLTRPC> 1134 
 COLTRPC2> 1251 

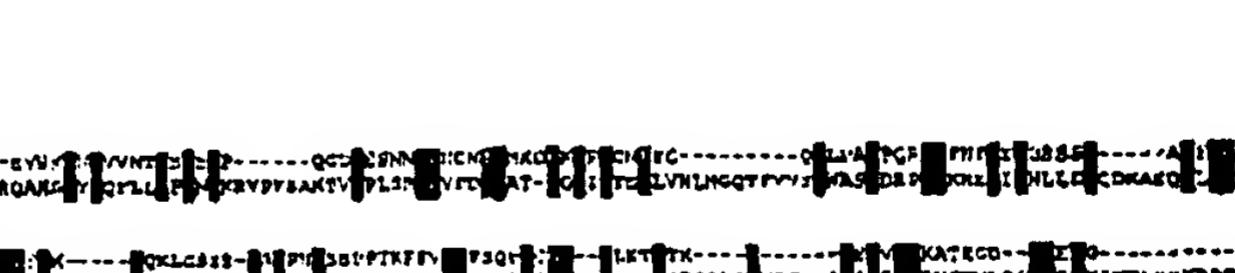
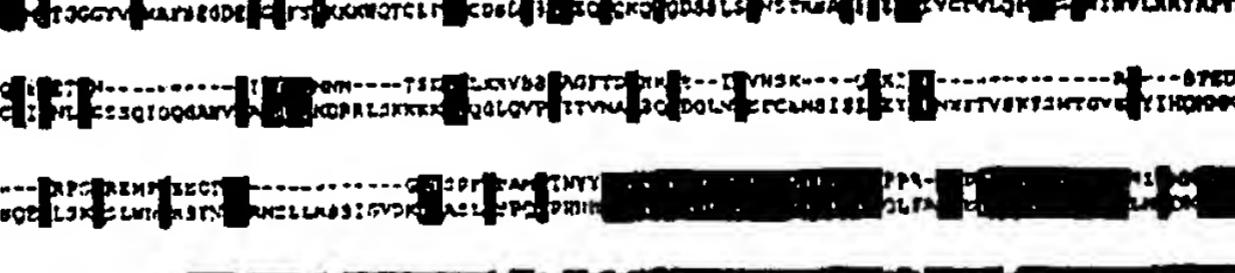
 MELANOMA_KINASE> 938 
 KIDNEY_KINASE> 670 
 LTRPC1_MTR1> 791 
 LTRPC2> 674 
 MELASTATIN> 713 
 LTRPC1_TRPC1> 732 
 DMLTRPC> 820 
 COLTRPC> 946 
 COLTRPC> 1197 
 COLTRPC2> 1198 

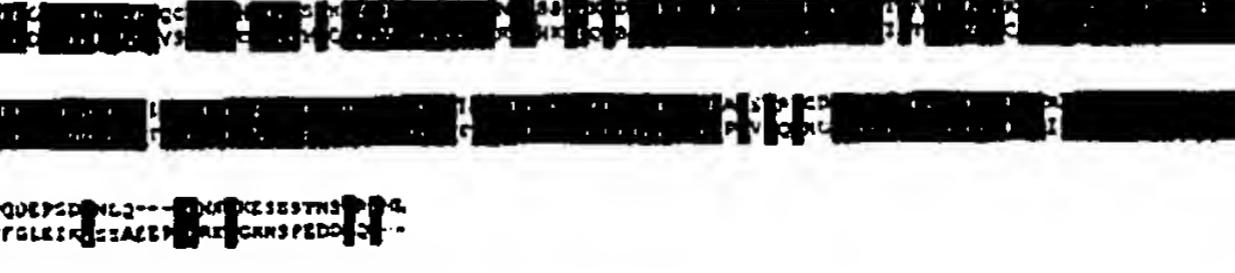
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 KIDNEY_KINASE> 971 
 LTRPC1_MTR1> 893 
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 MELASTATIN> 914 
 LTRPC1_TRPC1> 932 
 DMLTRPC> 980 
 COLTRPC> 1047 
 COLTRPC> 1296 
 COLTRPC2> 1297 

 MELANOMA_KINASE> 1352 
 KIDNEY_KINASE> 1025 
 LTRPC1_MTR1> 323 
 LTRPC2> 600 
 MELASTATIN> 249 
 LTRPC1_TRPC1> 383 
 DMLTRPC> 1089 
 COLTRPC> 1082 
 COLTRPC> 1320 
 COLTRPC2> 1284

 MELANOMA_KINASE> 1139 
 KIDNEY_KINASE> 1064 
 LTRPC1_MTR1> 1617 
 LTRPC2> 938 
 MELASTATIN> 1046 
 LTRPC1_TRPC1> 1387 
 DMLTRPC> 1172 
 COLTRPC> 1162 
 COLTRPC> 1423
 COLTRPC2> 1323

 MELANOMA_KINASE> 1234 
 KIDNEY_KINASE> 1186 
 LTRPC1_MTR1> 1111 
 LTRPC2> 1007 
 MELASTATIN> 1143 
 LTRPC1_TRPC1> 1188 
 DMLTRPC> 1273 
 COLTRPC> 1262
 COLTRPC> 1304
 COLTRPC2> 1415

 MELANOMA_KINASE> 1293 
 KIDNEY_KINASE> 1297 

 MELANOMA_KINASE> 1362 
 KIDNEY_KINASE> 1404 

 MELANOMA_KINASE> 1419 
 KIDNEY_KINASE> 1516 

 MELANOMA_KINASE> 1510
 KIDNEY_KINASE> 1624

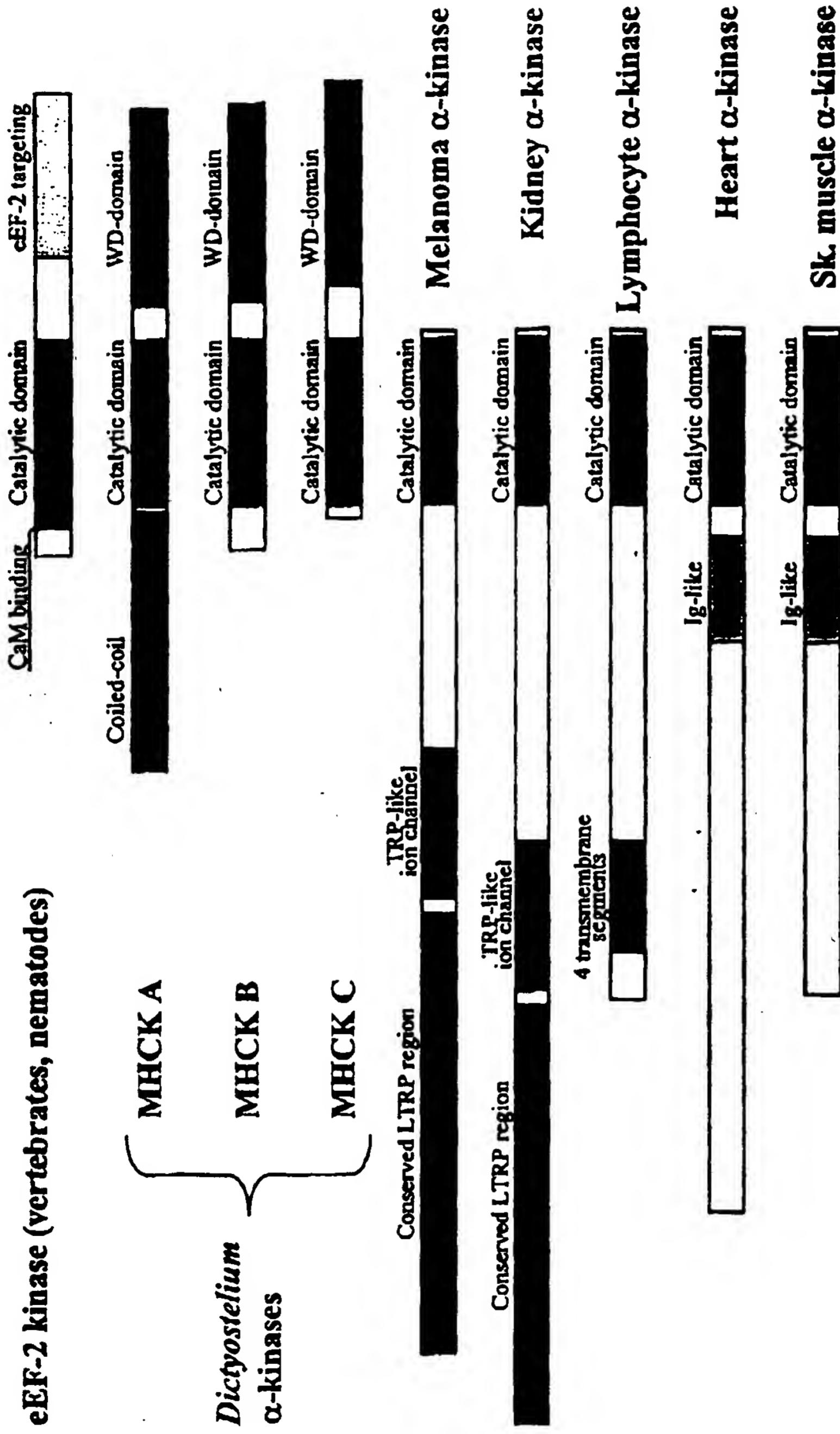
 MELANOMA_KINASE> 1693
 KIDNEY_KINASE> 1736

 MELANOMA_KINASE> 1713
 KIDNEY_KINASE> 1844

 MELANOMA_KINASE> 1872
 KIDNEY_KINASE> 1916

Figure 17

eEF-2 kinase (vertebrates, nematodes)



012860-1-109

18% of phys

Figure 18

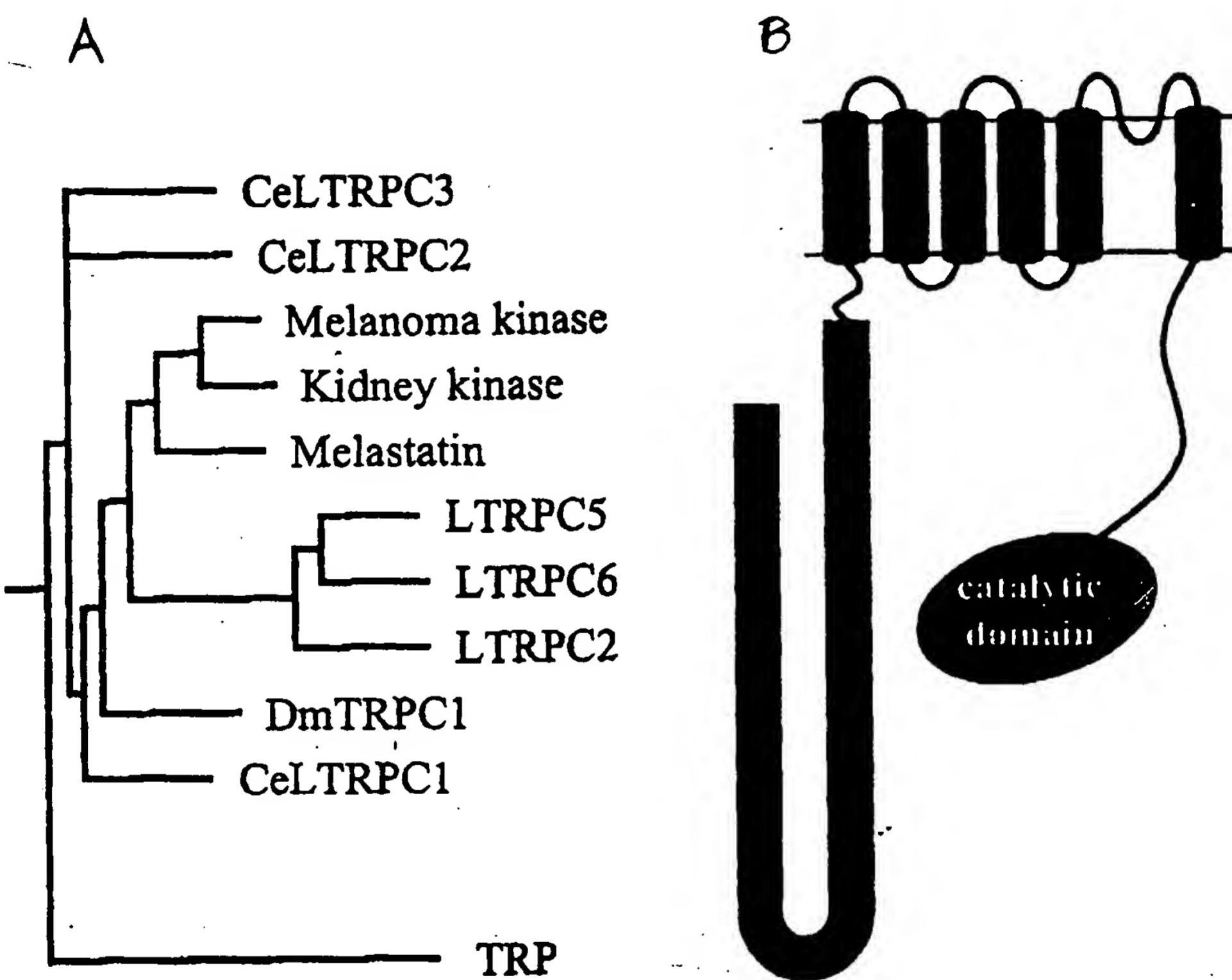


Figure 19A&B